

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2003, 07:42:15 / Search time 21 Seconds

(without alignments)
767.640 Million cell updates/sec

Title: US-09-623-035-2

Sequence: 1 MTVARPSVPAALPLGELPR.....HTCFTLTGLTLVTWGLLT 381

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 157478

Minimum DB seq length: 6
Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:
1: /cgn2_6/prodata/1/iaa/5A COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep:*
3: /cgn2_6/prodata/1/iaa/5A COMB.pep:*
4: /cgn2_6/prodata/1/iaa/5B COMB.pep:*
5: /cgn2_6/prodata/1/iaa/5A COMB.pep:*
6: /cgn2_6/prodata/1/iaa/5B COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	124	6.0	23	1	US-07-811-048-8
2	96	4.7	27	6	5256642-18
3	96	4.7	27	6	5472939-18
4	50.5	2.4	27	2	US-08-541-7598-5
5	48	2.3	26	1	US-08-450-360-12
6	47.5	2.3	27	2	US-08-441-7598-4
7	47.5	2.3	29	4	US-09-043-731-23
8	47	2.3	8	1	US-08-210-266A-4
9	47	2.3	8	1	US-08-688-675-4
10	47	2.3	8	3	US-08-477-860C-4
11	47	2.3	27	2	US-08-169-8488-22
12	47	2.3	27	2	US-08-448-873-22
13	47	2.3	27	2	US-08-382-452D-22
14	47	2.3	27	4	US-08-507-362A-10
15	46.5	2.3	26	2	US-08-288-059-2
16	46	2.2	27	2	US-08-541-7598-3
17	45	2.2	10	6	5378464-24
18	45	2.2	22	6	5378464-8
19	45	2.2	24	3	US-08-701-382-8
20	45	2.2	24	4	US-08-788-820-8
21	44.5	2.2	25	4	US-07-966-187-4
22	44.5	2.2	25	1	US-08-371-121-3
23	44.5	2.2	25	3	US-07-927-391-5
24	44.5	2.2	25	3	US-07-927-391-5
25	44	2.1	25	5	PCT-US94-04361-32
26	44	2.1	25	5	PCT-US94-04361-32
27	43.5	2.1	22	6	PCT-US94-04361-33

28	43.5	2.1	22	6	5472939-15	Patent No. 5472939
29	43.5	2.1	23	2	US-08-833-807-2	Sequence 2, Appl
30	43.5	2.1	23	3	US-09-223-043-2	Sequence 2, Appl
31	43.5	2.1	23	4	US-09-593-870A-2	Sequence 2, Appl
32	43	2.1	14	6	5256642-19	Patent No. 5256642
33	43	2.1	19	6	5472939-19	Patent No. 5472939
34	43	2.1	19	2	US-08-648-298-16	Sequence 16, Appl
35	43	2.1	25	4	US-09-439-313-520	Sequence 520, App
36	43	2.1	27	3	US-09-071-710-39	Sequence 39, Appl
37	43	2.1	27	3	US-09-525-397-39	Sequence 39, Appl
38	43	2.1	27	4	US-09-439-313-566	Sequence 566, App
39	43	2.1	29	4	US-09-439-313-546	Sequence 546, App
40	42	2.0	7	1	US-08-210-266A-5	Sequence 5, Appl
41	42	2.0	7	1	US-08-688-675-5	Sequence 5, Appl
42	42	2.0	7	3	US-08-477-860C-5	Sequence 39, Appl
43	41.5	2.0	16	1	US-08-151-219-1	Sequence 1, Appl
44	41.5	2.0	16	5	PCT-US94-13205-1	Sequence 1, Appl
45	41.5	2.0	25	5	PCT-US94-04361-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-07-811-048-8
Sequence 8, Application US/07811048

Patent No. 5264357

GENERAL INFORMATION: 11-1993

APPLICANT: Caras, Ingrid W.

TITLE OF INVENTION: Nucleic Acid and Methods for the Synthesis of No. 5264357el Fu

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/811,048

FILING DATE: 19911219

CLASSIFICATION: 530

PRIOR APPLICATION NO: 06/738171

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 06/859107

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: PCT/US86/01177

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Robert H.

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: 330P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/266-1489

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

US-07-811-048-8

Query Match 6.0%, Score 124, DB 1, Length 23;
Best Local Similarity 100.0%, Pred. No. 3, 1e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 35 DCGLPDVPVNAQALERTGTPP 56
DB 1 DCGLPDVPVNAQALERTGTPP 22

1, 11, 13, 34
055, 264, 357

RESULT 2

5256642-18
PATENT NO. 5256642
APPLICANT: PARON, DOUGLAS T.; KICKSTEIN, LLOYD B.; WONG,
MINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
RECEPTOR 1 (CR1) AND A THROMBOTIC AGENT, AND THE METHODS OF
USE THEREOF
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,128
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332,865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176,532
FILING DATE: 01-APR-1988
SEQ ID NO: 18
LENGTH: 27
5256642-18

Query Match 4.7%; Score 96; DB 6; Length 27;
Best Local Similarity 61.5%; Pred. No. 0.017;
Matches 16; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 257 FTMIGHSIYCTVNDGEGSGPPE 282
DB 2 FELVGEPSIYCTSDNDVGIMSGPAPQ 27

RESULT 3

5472939-18
PATENT NO. 5472939
APPLICANT: PARON, DOUGLAS T.; KICKSTEIN, LLOYD B.; WONG,
MINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
MEDIATED DISORDERS
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,825
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 588,128
FILING DATE: 24-SEP-1990
APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332,865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176,532
FILING DATE: 01-APR-1988
SEQ ID NO: 18
LENGTH: 27
5472939-18

Query Match 4.7%; Score 96; DB 6; Length 27;
Best Local Similarity 61.5%; Pred. No. 0.017;
Matches 16; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 257 FTMIGHSIYCTVNDGEGSGPPE 282
DB 2 FELVGEPSIYCTSDNDVGIMSGPAPQ 27

RESULT 4
US-08-541-759B-5
Sequence 5, Application US/08541759B
Patent No. 586160

GENERAL INFORMATION:
APPLICANT: Quick, Douglas P.
APPLICANT: Welter, Mark W.
APPLICANT: Welter, Joseph
APPLICANT: Welter, Lisa M.
TITLE OF INVENTION: ISOSPORA SUIIS VACCINE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Akzo No. 586160el Patent Dept.
STREET: 1300 Piccard Drive, Suite 206
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,759B
FILING DATE: 10-OCT-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kleener, Sharon N.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: 36,335
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-948-9751
FAX: 301-948-7400

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-541-759B-5

Query Match 2.4%; Score 50.5; DB 2; Length 27;
Best Local Similarity 41.4%; Pred. No. 3.3e+02;
Matches 12; Conservative 4; Mismatches 8; Indels 5; Gaps 1;

QY 292 VPPTVOKPTTVNPTTEVSPTSQKTTKT 320
DB 1 VPPTTEVP-----PTEEVTPPTGCTPPT 24

RESULT 5

US-08-450-360-12
Sequence 12, Application US/08450360
Patent No. 5656457
GENERAL INFORMATION:
APPLICANT: Parkes, Deborah Lynn
APPLICANT: Coates, Stephen Ralph
TITLE OF INVENTION: Herpes Simplex Virus Type 2-Glycoprotein G
TITLE OF INVENTION: Proteins and Polypeptides
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2003, 07:42:11 (Search time 49 seconds)

(without alignments)
1234.180 Million cell updates/sec

Title: US-09-623-035-2
Perfect score: 2064

Sequence: 1 MTVARPSVPALPLGLGELPR.....HRCFTLTGLTGLTVMGLLT 381

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 436344

Minimum DB seq length: 6
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

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- 4: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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- 22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
- 23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	7.1	29	15	AAR50086
2	89.5	4.3	28	23	AAAM50805
3	64.5	3.1	23	18	AAAM1838
4	61	3.0	10	22	AAAG7023
5	58	2.8	10	22	AAAG7081
6	58	2.8	10	22	AAAG7083
7	57	2.8	10	22	AAAG7043
8	55	2.7	10	22	AAAG7037
9	55	2.7	10	22	AAAG7045

10	54	2.6	10	22	AAAG7089	Human complement
11	52.5	2.5	19	21	AAAG6634	Oestrogen receptor
12	52.5	2.5	19	23	AAU86371	Oestrogen receptor
13	52	2.5	10	22	AAAG96997	Human complement
14	52	2.5	10	22	AAAG7001	Human complement
15	52	2.5	10	22	AAAG7015	Human complement
16	52	2.5	10	22	AAAG7059	Human complement
17	52	2.5	10	22	AAAG7091	Human complement
18	51.5	2.5	27	24	ABU07673	Human complement
19	51	2.5	10	22	AAAG6999	Human complement
20	51	2.5	10	22	AAAG7003	Human complement
21	51	2.5	10	22	AAAG7005	Human complement
22	51	2.5	10	22	AAAG7007	Human complement
23	51	2.5	10	22	AAAG7011	Human complement
24	51	2.5	10	22	AAAG7017	Human complement
25	51	2.5	10	22	AAAG7013	Human complement
26	51	2.5	10	22	AAAG7017	Human complement
27	51	2.5	10	22	AAAG7031	Human complement
28	51	2.5	10	22	AAAG7033	Human complement
29	51	2.5	10	22	AAAG7041	Human complement
30	51	2.5	10	22	AAAG7049	Human complement
31	51	2.5	10	22	AAAG7051	Human complement
32	51	2.5	10	22	AAAG7053	Human complement
33	51	2.5	10	22	AAAG7055	Human complement
34	51	2.5	10	22	AAAG7069	Human complement
35	51	2.5	10	22	AAAG7071	Human complement
36	51	2.5	10	22	AAAG7073	Human complement
37	51	2.5	10	22	AAAG7075	Human complement
38	51	2.5	10	22	AAAG7077	Human complement
39	51	2.5	10	22	AAAG7079	Human complement
40	51	2.5	10	22	AAAG7085	Human complement
41	51	2.5	10	22	AAAG7093	Human complement
42	51	2.5	10	22	AAAG7095	Human complement
43	51	2.5	10	22	AAAG7097	Human complement
44	51	2.5	10	22	AAAG7105	Human complement
45	51	2.5	10	22	AAAG7107	Human complement

ALIGNMENTS.

RESULT 1					
AAAR50086	AAAR50086 standard; Protein, 29 AA.				
XX					
AC	AAAR50086;				
XX					
DT	25-MAR-2003 (updated)				
DT	27-OCT-1994 (first entry)				
XX					
DE	Decay accelerating factor derived attachment signal.				
XX					
KW	Fusion protein; xenograft; transplacental; membrane; transplacental;				
KW	membrane cofactor protein; MCP; decay accelerating factor; DAF; GPI;				
KW	glycophosphatidyl inositol; anchor; intermembrane transfer				
OS	Homo sapiens.				
XX					
FT	Key				
FT	Domain				
XX					
XX	MO9406903=A1				
XX					
PD	31-MAR-1994.				
XX					
PF	22-SEP-1993; 93WO-US08889.				
XX					
PR	22-SEP-1992; 92US-0948521.				
XX					
PA	(DNXB-) DNK BIOTHERAPEUTICS INC.				
XX					
PI	Byrne GW, Kooyman DL, Logan JS;				

Location/Qualifiers
13..29 /note="C-terminal hydrophobic domain."

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XX WPI; 1994-118454/14.
 XX Delivery of proteins, using mobile cell, by intermembrane
 PT transfer - for pre-accommodation of xenogeneic organ transplants
 XX disclosure; Page 43; 104pp; English.
 XX A protein of interest may be delivered to the tissue of a target
 CC animal by providing mobile cells which bear the protein on their
 CC membrane, linked to a glycoposphatidyl inositol (GPI) anchor. The
 CC cells circulate in the target animal, coming into contact with the
 CC tissue and transfer the protein to the tissue by intermembrane
 CC transfer. Intermembrane transfer by this method occurs at a greater
 CC rate than naturally in the animal. This sequence is an attachment
 CC signal derived from decay accelerating factor (DAF). DAF is
 CC naturally GPI linked. Preferably, the protein of interest is
 CC expressed as a fusion product, the fusion protein comprising this
 CC sequence and the protein (or fragment) of interest. The method is
 CC especially useful for modifying pig organs for xenotransplantation
 CC into humans. See AAO58894.
 CC (Updated on 25-MAR-2003 to correct PW field.)
 CC
 CC Sequence 29 AA:
 SQ

Query Match 7.1%; Score 147; DB 15; Length 29;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 353 SGTTRLLSGHTCTFLTGILGLVWGLLT 381
 DB 1 SGTTRLLSGHTCTFLTGILGLVWGLLT 29

1, 11, 13, 34

RESULT 2
 AAMS0805
 ID AAMS0805 standard; Peptide; 28 AA.
 XX
 AC AAMS0805;
 XX
 DT 01-MAY-2002 (first entry)
 XX
 DE Human complement receptor type 1 tryptic peptide 54d.
 XX
 KW Complement receptor type 1; CRI; C3b/C4b receptor; human;
 KW inflammation; myocardial infarction; reperfusion injury;
 KW antiinflammatory; therapy; diagnosis; receptor; purification.
 XX
 OS Homo sapiens.
 XX
 PN US6316604-B1.
 PD 13-NOV-2001.
 XX
 PF 05-JUN-1995; 95US-0463959.
 XX
 PR 03-APR-1989; 89US-0332865.
 PR 06-DEC-1994; 94US-0350238.
 PR 24-FEB-1993; 93US-0026134.
 PR 01-APR-1988; 88US-0176532.
 XX
 PA (AVANT-) AVANT IMMUNOTHERAPEUTICS INC.
 XX
 PI Fearon DT, Klickstein LB, Wong WW, Carson GR, Concino MF, Ip SH;
 PI Makrides SC, Marsh HC;
 XX
 DR WPI; 2002-121028/16.
 XX
 CC Purifying a recombinant soluble complement receptor type 1 molecule or
 CC fragment, useful for diagnosing or treating disorders associated
 CC with complement activity, using cation exchange chromatography provides

PS Example; Column 25; 44pp; English.

XX The present sequence is that of tryptic peptide 54d of human
 CC erythrocyte C3b/C4b receptor CRI (complement receptor type 1).
 CC The peptide corresponds to amino acids 204-231 and 654-681 of a
 CC full-length CRI sequence (see AAM50797) predicted from isolated cDNA
 CC clones. The invention provides recombinant, soluble CRI polypeptides
 CC that lack the transmembrane domain of the native protein, and methods
 CC of purifying them. CRI polypeptides and nucleic acids have use in
 CC the diagnosis and therapy of disorders involving complement activity
 CC and various immune system or inflammatory disorders. Secreted,
 CC recombinant CRI has been produced in large quantities using CHO host
 CC cells grown in serum-free medium. The purified protein was used to
 CC reduce damage caused by inflammation, and to reduce myocardial
 CC infarct size and prevent reperfusion injury in rats.

XX Sequence 28 AA;

Query Match 4.3%; Score 89.5; DB 23; Length 28;
 Best Local Similarity 59.3%; Pred. No. 3.9;
 Matches 16; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

QY 257 FTWIGHSIYCTVNDDE-GEWSCPPE 282
 DB 2 FELVGEPSIYCTSDNDQVIGMSGAPQ 28

RESULT 3
 AAM31838
 ID AAM31838 standard; peptide; 23 AA.
 XX
 AC AAM31838;
 XX
 DT 26-MAR-1998 (first entry)
 XX
 DE Peptide 4 from the short consensus repeat 3 of complement receptor 1.

XX Short consensus repeat 3; long homologous repeat A; LHR-A;
 KW complement receptor 1; CRI; complement inhibition;
 KW anti-haemolytic activity; inflammation; thrombotic condition;
 KW inappropriate complement activation; ARDS; Alzheimer's disease.
 XX
 OS Synthetic.
 XX
 PN WO9731944-A1.
 PD 04-SEP-1997.
 XX
 PF 26-FEB-1997; 97WO-EP00994.
 XX
 PR 02-MAR-1996; 96GB-0004518.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Edge CM, Mossakowska DEI, Smith RAG;
 XX
 DR WPI; 1997-448630/41.
 XX
 CC Synthetic soluble peptides AAM31835-38 are derived from the short
 CC consensus repeat 3 of the long homologous repeat A (LHR-A) of human
 CC complement receptor 1 (CRI). The present peptide is located between
 CC residues 164 and 186. These peptides have functional complement
 CC inhibitory, including anti-haemolytic, activity. Enhanced activity
 CC may be achieved by linking the peptides to a core structure
 CC (e.g. the MAP peptide) to produce a multimeric or chimeric polypeptide.

This Page Blank (uspto)

SOFTWARE: Patentln Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,360
FILING DATE: 25-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/129,021
FILING DATE: 29-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0012.2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-450-360-12

Query Match 2.3%; Score 48; DB 1; Length 26;
Best Local Similarity 41.7%; Pred. No. 54e+02;
Matches 10; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 311 PTSQKTTKTTTPNAQATRSTPVS 334
Db 1 PTTTHATPPTTPGQTPPGPAT 24

RESULT 6
US-08-541-759B-4
Sequence 4, Application US/08541759B
Patent No. 5861160
GENERAL INFORMATION:
APPLICANT: Quick, Douglas P.
APPLICANT: Welter, Mark W.
APPLICANT: Welter, Joseph
APPLICANT: Welter, Lisa M.
TITLE OF INVENTION: ISOSPORA SUIIS VACCINE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 5861160el Patent Dept.
STREET: 1300 Piccard Drive, Suite 206
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,759B
FILING DATE: 10-OCT-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Klesner, Sharon N.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: Quick1a
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-948-9751
TELEFAX: 301-948-7400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-541-759B-4

Query Match 2.3%; Score 47.5; DB 2; Length 27;
Best Local Similarity 37.9%; Pred. No. 6.3e+02;
Matches 11; Conservative 5; Mismatches 8; Indels 5; Gaps 1;

QY 292 VPPTQKPTTVNVPTEVSPTSQKTTT 320
Db 1 LPTEVP-----PTEVTPTEGETPPT 24

RESULT 7
US-09-043-731-23
Sequence 23, Application US/09043731A
Patent No. 6344203
GENERAL INFORMATION:
APPLICANT: The Austin Research Institute
TITLE OF INVENTION: Mimicking Peptides in Cancer Therapy
FILE REFERENCE: CALA-200
CURRENT APPLICATION NUMBER: US/09/043,731A
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 23
LENGTH: 29
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: single
US-09-043-731-23

Query Match 2.3%; Score 47.5; DB 4; Length 29;
Best Local Similarity 48.0%; Pred. No. 7e+02;
Matches 12; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 299 PTTVNVPTTE-VSPISQKTTT 322
Db 3 PTTTPISTTVVTPPTPTPTPTPT 27

RESULT 8
US-08-210-266A-4
Sequence 4, Application US/08210266A
Patent No. 5545619
GENERAL INFORMATION:
APPLICANT: Atkinson, John P.
APPLICANT: Hourcade, Dennis
APPLICANT: Krych, Malgorzata
TITLE OF INVENTION: Modified Complement System
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree
STREET: Street
CITY: Atlanta
STATE: Georgia
COUNTRY: US
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/210,266A
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/695,514
FILING DATE: 03-MAY-1991
ATTORNEY/AGENT INFORMATION:

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NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)873-8794
TELEFAX: (404)873-8794
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-210-266A-4

Query Match 2.3%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 SDPLPECR 221
Db 1 SDPLPECR 8 1, 34

RESULT 9
US-08-688-675-4
Sequence 4, Application US/08688675
Patent No. 5719127
GENERAL INFORMATION:
APPLICANT: Atkinson, John P.
APPLICANT: Hourcade, Dennis
APPLICANT: Krych, Malgorzata
TITLE OF INVENTION: Modified Complement System Regulators
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree
STREET: Street
CITY: Atlanta
STATE: Georgia
COUNTRY: US
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/688,675
FILING DATE: 30-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/210,266
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/695,514
FILING DATE: 03-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU101div2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)873-8794
TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-688-675-4

2.3%; Score 47; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 SDPLPECR 221
Db 1 SDPLPECR 8

RESULT 10
US-08-477-860C-4
Sequence 4, Application US/08477860C
Patent No. 6010873
GENERAL INFORMATION:
APPLICANT: Atkinson, John P.
APPLICANT: Hourcade, Dennis
APPLICANT: Krych, Malgorzata
TITLE OF INVENTION: Modified Complement System Regulators
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree
STREET: Street
CITY: Atlanta
STATE: Georgia
COUNTRY: US
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,860C
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/210,266
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/695,514
FILING DATE: 03-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU 101 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)873-8794
TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-860C-4

Query Match 2.3%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 SDPLPECR 221
Db 1 SDPLPECR 8

RESULT 11
US-08-169-948B-22
Sequence 22, Application US/08169948B
Patent No. 5861271
GENERAL INFORMATION:
APPLICANT: Fowler, Timothy
APPLICANT: Ward, Michael
APPLICANT: Clarkson, Kathleen

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2003, 07:42:15 ; Search time 21 Seconds
(without alignments)
767.640 Million cell updates/sec

Title: US-09-623-035-2

Perfect score: 2064

Sequence: 1 MVARPSVPAALLGELPR.....HTCFTLTGLLTVMGLLT 381

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 157478

Minimum DB seq length: 6

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/PCITUS_COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	124	6.0	23	1	US-07-811-048-8
2	96	4.7	27	6	Sequence 8, Appli
3	96	4.7	27	6	Patent No. 5256642
4	50.5	2.4	27	2	US-07-811-048-8
5	48	2.3	26	1	US-08-541-759B-5
6	47.5	2.3	27	2	US-08-450-360-12
7	47.5	2.3	27	2	US-08-541-759B-4
8	47	2.3	29	4	US-09-043-731-23
9	47	2.3	8	1	US-08-210-266A-4
10	47	2.3	8	3	US-08-688-675-4
11	47	2.3	8	3	US-08-477-860C-4
12	47	2.3	27	2	US-08-169-948B-22
13	47	2.3	27	2	US-08-448-873-22
14	47	2.3	27	3	US-08-382-452D-22
15	46.5	2.3	26	2	US-08-507-362A-10
16	46	2.2	27	2	US-08-288-059-2
17	45	2.2	27	2	US-08-541-759B-3
18	45	2.2	22	6	5378464-24
19	45	2.2	22	6	5378464-8
20	45	2.2	24	3	US-08-701-382-8
21	44.5	2.2	24	4	US-08-788-820-8
22	44.5	2.2	25	1	US-07-966-187-4
23	44.5	2.2	25	1	US-08-371-121-3
24	44.5	2.2	25	3	US-07-927-391-5
25	44	2.1	22	5	PCT-US94-04361-32
26	44	2.1	22	4	US-09-461-325-488
27	43.5	2.1	22	5	PCT-US94-04361-33
			22	6	5256642-15

28	43.5	2.1	22	6	5472939-15	Patent No. 5472939
29	43.5	2.1	23	2	US-08-833-807-2	Sequence 2, Appli
30	43.5	2.1	23	3	US-09-223-043-2	Sequence 2, Appli
31	43.5	2.1	23	4	US-09-593-870A-2	Sequence 2, Appli
32	43	2.1	14	6	5256642-19	Patent No. 5256642
33	43	2.1	14	6	5472939-19	Patent No. 5472939
34	43	2.1	19	2	US-08-648-298-16	Sequence 16, Appli
35	43	2.1	25	4	US-09-439-313-520	Sequence 520, App
36	43	2.1	27	3	US-09-071-710-39	Sequence 39, Appli
37	43	2.1	27	3	US-09-525-397-39	Sequence 39, Appli
38	43	2.1	27	4	US-09-439-313-566	Sequence 566, App
39	43	2.1	29	4	US-09-439-313-546	Sequence 546, App
40	42	2.0	7	1	US-08-210-266A-5	Sequence 5, Appli
41	42	2.0	7	1	US-08-688-675-5	Sequence 5, Appli
42	42	2.0	7	3	US-08-477-860C-5	Sequence 5, Appli
43	41.5	2.0	16	1	US-08-151-219-1	Sequence 1, Appli
44	41.5	2.0	16	5	PCT-US94-13205-1	Sequence 1, Appli
45	41.5	2.0	25	5	PCT-US94-04361-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1

US-07-811-048-8

; Sequence 8, Application US/07811048

; Patent No. 5264357

; GENERAL INFORMATION:

; APPLICANT: Caras, Ingrid W.

; TITLE OF INVENTION: Nucleic Acid and Methods for the Synthesis of No. 5264357e1 Fur

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/811,048

; FILING DATE: 19911219

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 06/738171

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 06/859107

; PRIOR APPLICATION DATA: PCT/US86/01177

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/083757

; ATTORNEY/AGENT INFORMATION:

; NAME: Benson, Robert H.

; REGISTRATION NUMBER: 30,446

; REFERENCE/DOCKET NUMBER: 330p1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/266-1489

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 23 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; US-07-811-048-8

Query Match 6.0%; Score 124; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	35	DCGLPPDPVNAQPALEGRTSFF	56
D6	1	DCGLPPDPVNAQPALEGRTSFF	22

1, 11, 13, 34

RESULT 2
5256642-18
; Patent No. 5256642
; APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
; WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
; H.; MAKRIODES, SAVVAS; MARSH, HENRY C. JR.
; TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
; RECEPTOR 1 (CR1) AND A THROMBOLYTIC AGENT, AND THE METHODS OF
; USE THEREOF OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,128
; FILING DATE: 24-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 412,745
; FILING DATE: 26-SEP-1989
; APPLICATION NUMBER: 332,865
; FILING DATE: 03-APR-1989
; APPLICATION NUMBER: 176,532
; FILING DATE: 01-APR-1988
; SEQ ID NO:18:
; LENGTH: 27
5256642-18

Query Match	4.7%	Score 96;	DB 6;	Length 27;
Best Local Similarity	61.3%;	Pred. No. 0.017;		
Matches 16;	Conservative 4;	Mismatches 6;	Indels 0;	Gaps 0;
QY	257	FTMIGHSIYCTVNNDEGWSGPPPE	282	
		: :		
Db	2	FELVGEPSIYCTSNDDVGWSGPAQ	27	

RESULT 3
5472939-18
; Patent NO. 5472939
; APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
; WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
; H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
; TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
; MEDIATED DISORDERS
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/138,825
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 588,128
; FILING DATE: 24-SEP-1990
; APPLICATION NUMBER: 412,745
; FILING DATE: 26-SEP-1989
; APPLICATION NUMBER: 332,865
; FILING DATE: 03-APR-1989
; APPLICATION NUMBER: 176,532
; FILING DATE: 01-APR-1988
; SEQ ID NO: 18:
; LENGTH: 27

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Query Match      4.7%; Score 96; DB 6; Length 27;
Best Local Similarity 61.5%; Pred. No. 0.017;
Matches 16; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      257 FTWIGHSIHYCTVNNDEGEWSGGPPE 282
      | : : | | | | | | | | | | :
Db      2 FRLVGGPSIVCTSNDDVGIWSGPAQ 27

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RESULT 4
US-08-541-759B-5
; Sequence 5, Application US/08541759B
; Patent No. 5861160
; GENERAL INFORMATION:
; APPLICANT: Quick, Douglas P.
; APPLICANT: Welter, Mark W.
; APPLICANT: Welter, Joseph
; APPLICANT: Welter, Lisa M.
; TITLE OF INVENTION: ISOSPOR A SUI S VACCINE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5861160el Patent Dept.
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541.759B
; FILING DATE: 10-OCT-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Klesner, Sharon N.
; REGISTRATION NUMBER: 36,335
; REFERENCE/DOCKET NUMBER: Quickla
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-948-7400
; TELEFAX: 301-948-9751
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-541-759B-5

```

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Query Match      2.4%; Score 50.5; DB 2; Length 27;
Best Local Similarity 41.4%; Pred. No. 3.3e+02;
Matches 12; Conservative 4; Mismatches 8; Indels 5; Gaps 1;

QY 292 VPPTVQKPTTVNVPTTEVSPTSQKTTTKT 320
      ||||| : ||| : :
Db 1 VPPTTEVP-----PTEEVTPPTTEGTPPT 24

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RESULT 5
US-08-450-360-12
; Sequence 12, Application US/08450360
; Patent No. 5656457
; GENERAL INFORMATION:
; APPLICANT: Parkes, Deborah Lynn
; APPLICANT: Coates, Stephen Ralph
; TITLE OF INVENTION: Herpes Simplex Virus Type 2-Glycoprotein G
; TITLE OF INVENTION: Proteins and Polypeptides
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/450,360

;; FILING DATE: 25-MAY-1995

;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/129,021

;; FILING DATE: 29-SEP-1993

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Lauder, Leona L.

;; REGISTRATION NUMBER: 30,863

;; REFERENCE/DOCKET NUMBER: D-0012.2A

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 415-435-2034

;; TELEFAX: 415-435-0727

;; GENERAL INFORMATION:

;; INFORMATION FOR SEQ ID NO: 12:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 26 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: peptide

;; US-08-450-360-12

Query Match 2.3%; Score 48; DB 1; Length 26;
Best Local Similarity 41.7%; Pred. No. 5.4e+02;
Matches 10; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 311 PTSQKTTTTPNAQATSTPVS 334

Db 1 PSTHTATPRTTGPQTTPGPAT 24

RESULT 6

US-08-541-759B-4

;; Sequence 4, Application US/08541759B

;; Patent No. 5861160

;; GENERAL INFORMATION:

;; APPLICANT: Quick, Douglas P.

;; APPLICANT: Welter, Mark W.

;; APPLICANT: Welter, Joseph

;; APPLICANT: Welter, Lisa M.

;; TITLE OF INVENTION: ISOSPORA SUIIS VACCINE

;; NUMBER OF SEQUENCES: 11

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Akzo No. 5861160el Patent Dept.

;; STREET: 1300 Piccard Drive, Suite 206

;; CITY: Rockville

;; STATE: Maryland

;; COUNTRY: USA

;; ZIP: 20850

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/541,759B

;; FILING DATE: 10-OCT-1995

;; CLASSIFICATION: 424

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Klesner, Sharon N.

;; REGISTRATION NUMBER: 36,335

;; REFERENCE/DOCKET NUMBER: Quickla

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 301-948-7400

;; TELEFAX: 301-948-9751

;; INFORMATION FOR SEQ ID NO: 4:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 27 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;;

;;

;;

;;

;;

;;

;;

;;

;; MOLECULE TYPE: peptide

;; US-08-541-759B-4

Query Match 2.3%; Score 47.5; DB 2; Length 27;

Best Local Similarity 37.9%; Pred. No. 6.3e+02;

Matches 11; Conservative 5; Mismatches 8; Indels 5; Gaps 1;

QY 292 VPPTVQKPTTVNVPTTEVSPTSQKTTTKT 320

Db 1 LPPTTEVP-----PTEEVTPPTGETPPT 24

RESULT 7

US-09-043-731-23

;; Sequence 23, Application US/09043731A

;; Patent No. 6344203

;; GENERAL INFORMATION:

;; APPLICANT: The Austin Research Institute

;; TITLE OF INVENTION: Mimicking Peptides in Cancer Therapy

;; FILE REFERENCE: CALA-200

;; CURRENT APPLICATION NUMBER: US/09/043,731A

;; CURRENT FILING DATE: 1998-06-23

;; NUMBER OF SEQ ID NOS: 26

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 23

;; LENGTH: 29

;; TYPE: PRT

;; ORGANISM: Artificial Sequence

;; FEATURE:

;; OTHER INFORMATION: Description of Artificial Sequence: single

;; OTHER INFORMATION: stranded linear peptide

;; US-09-043-731-23

Query Match 2.3%; Score 47.5; DB 4; Length 29;

Best Local Similarity 48.0%; Pred. No. 7e+02;

Matches 12; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 299 PTTNVVPTTE-VSPTSQKTTT 322

Db 3 PTTTISITTTVMVTPPTPTGTGTPT 27

RESULT 8

US-08-210-266A-4

;; Sequence 4, Application US/08210266A

;; Patent No. 5545619

;; GENERAL INFORMATION:

;; APPLICANT: Atkinson, John P.

;; APPLICANT: Hourcade, Dennis

;; APPLICANT: Krych, Malgorzata

;; TITLE OF INVENTION: Modified Complement System

;; TITLE OF INVENTION: Regulators

;; NUMBER OF SEQUENCES: 18

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Patrea L. Pabst

;; STREET: 2800 One Atlantic Center, 1201 West Peachtree.

;; CITY: Atlanta

;; STATE: Georgia

;; COUNTRY: US

;; ZIP: 30309-3450

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/210,266A

;; FILING DATE: 18-MAR-1994

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/695,514

;; FILING DATE: 03-MAY-1991

;; ATTORNEY/AGENT INFORMATION:

;;

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;;

;;

;;

;;

;;

;;

NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU101
TELEPHONE: (404)873-8794
TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-210-266A-4

Query Match 2.3%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 SDPLPCR 221
Db 1 SDPLPCR 8

RESULT 9
US-08-688-675-4
Sequence 4, Application US/08688675
Patent No. 5719127
GENERAL INFORMATION:
APPLICANT: Atkinson, John P.
APPLICANT: Hourcade, Dennis
APPLICANT: Krych, Malgorzata
TITLE OF INVENTION: Modified Complement System Regulators
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree
CITY: Atlanta
STATE: Georgia
COUNTRY: US
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 30-JUN-1996
PRIOR APPLICATION NUMBER: US/08/688,675
FILING DATE: 03-MAY-1991
APPLICATION NUMBER: US 08/210,266
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 07/695,514
FILING DATE: 03-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU101div2
TELEPHONE: (404)873-8794
TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-688-675-4

Query Match 2.3%; Score 47; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 SDPLPCR 221
Db 1 SDPLPCR 8

RESULT 10
US-08-477-860C-4
Sequence 4, Application US/08477860C
Patent No. 6010873
GENERAL INFORMATION:
APPLICANT: Atkinson, John P.
APPLICANT: Hourcade, Dennis
APPLICANT: Krych, Malgorzata
TITLE OF INVENTION: Modified Complement System Regulators
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree
CITY: Atlanta
STATE: Georgia
COUNTRY: US
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 7-JUN-1995
PRIOR APPLICATION NUMBER: US/08/477,860C
FILING DATE: 18-MAR-1994
APPLICATION NUMBER: US 08/210,266
FILING DATE: 03-MAY-1991
APPLICATION NUMBER: US 07/695,514
FILING DATE: 03-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU 101 DIV
TELEPHONE: (404)873-8794
TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-860C-4

Query Match 2.3%; Score 47; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 SDPLPCR 221
Db 1 SDPLPCR 8

RESULT 11
US-08-169-948B-22
Sequence 22, Application US/08169948B
Patent No. 5861271
GENERAL INFORMATION:
APPLICANT: Fowler, Timothy
APPLICANT: Ward, Michael
APPLICANT: Clarkson, Kathleen

APPLICANT: Collier, Katherine
APPLICANT: Larenas, Edmund
TITLE OF INVENTION: No. 5861271el Cellulase Enzymes and Systems
TITLE OF INVENTION: For Their Expression
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/169,948B
FILING DATE: DEC 17 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Horn, Margaret A.
REGISTRATION NUMBER: 33,401
REFERENCE/DOCKET NUMBER: GC226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7536
TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-169-948B-22

Query Match 2.3%; Score 47; DB 2; Length 27;
Best Local Similarity 40.9%; Pred. No. 7.1e+02;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 311 PTSQKTTTKTTPNAQATRSTP 332
Db 1 PPPASSTTFSTPRSTSSSP 22

RESULT 12
US-08-448-873-22
Sequence 22, Application US/08448873
Patent No. 5874276
GENERAL INFORMATION:
APPLICANT: Fowler, Timothy
APPLICANT: Ward, Michael
APPLICANT: Clarkson, Kathleen
APPLICANT: Collier, Katherine A.
APPLICANT: Larenas, Edmund
TITLE OF INVENTION: No. 5874276el Cellulase Enzymes and Systems
TITLE OF INVENTION: For Their Expressions
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,873
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/169,948
FILING DATE: 17-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Christopher L.
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC226D14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7555
TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-448-873-22

Query Match 2.3%; Score 47; DB 2; Length 27;
Best Local Similarity 40.9%; Pred. No. 7.1e+02;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 311 PTSQKTTTKTTPNAQATRSTP 332
Db 1 PPPASSTTFSTPRSTSSSP 22

RESULT 13
US-08-382-452D-22
Sequence 22, Application US/08382452D
Patent No. 6268196
GENERAL INFORMATION:
APPLICANT: Fowler, Timothy
APPLICANT: Clarkson, Kathleen A.
APPLICANT: Ward, Michael
APPLICANT: Collier, Katherine D.
APPLICANT: Larenas, Edmund A.
TITLE OF INVENTION: NOVEL CELLULOSE ENZYMES AND SYSTEMS
TITLE OF INVENTION: FOR THEIR EXPRESSION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/382,452D
FILING DATE: February 1, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Christopher L. Stone
REGISTRATION NUMBER: 36,696
REFERENCE/DOCKET NUMBER: GC226-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7555
TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-382-452D-22

Query Match 2.3%; Score 47; DB 3; Length 27;
Best Local Similarity 40.9%; Pred. No. 7.1e+02;

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARB Y & CUSHMAN, L.L.P.
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,059
FILING DATE: 08-AUG-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CHAPIN, MARLANA K.
REGISTRATION NUMBER: 35,843
REFERENCE/DOCKET NUMBER: 61137/205204
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3711
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-288-059-2
Query Match 2.3%; Score 46.5; DB 2; Length 26;
Best Local Similarity 50.0%; Pred. No. 7.5e+02;
Matches 12; Conservative 2; Mismatches 9; Indels

Qy 299 PTTVNV-PTTEVSPTSQKTTTKT 321
||| : ||| : |||
Db 1 PTTPTTTTIVIPPTPTPTGTT 24

Search completed: November 18, 2003, 07:44:07
Job time : 22 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2003, 07:42:11 ; Search time 49 Seconds
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Title: US-09-623-035-2

Perfect score: 2064

Sequence: 1 MTVPSPVPAALPLLGELPR.....HTCFTLTGLLTGTLVTWGLLT 381

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 436344

Minimum DB seq length: 6

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	7.1	29	15	Decay accelerating
2	89.5	4.3	28	23	Human complement r
3	64.5	3.1	23	18	Peptide 4 from the
4	61	3.0	10	22	Human complementar
5	58	2.8	10	22	Human complementar
6	58	2.8	10	22	Human complementar
7	57	2.8	10	22	Human complementar
8	55	2.7	10	22	Human complementar
9	55	2.7	10	22	Human complementar

10	54	2.6	10	22	AAG97089	Human complementar
11	52.5	2.5	19	21	AAU65634	Oestrogen receptor
12	52.5	2.5	19	23	AAU86371	Oestrogen receptor
13	52	2.5	10	22	AAG96997	Human complementar
14	52	2.5	10	22	AAG97001	Human complementar
15	52	2.5	10	22	AAG97015	Human complementar
16	52	2.5	10	22	AAG97059	Human complementar
17	52	2.5	10	22	AAG97091	Human complementar
18	51.5	2.5	27	24	ABU07673	Human haptogloblin
19	51	2.5	10	22	AAG96999	Human complementar
20	51	2.5	10	22	AAG97003	Human complementar
21	51	2.5	10	22	AAG97005	Human complementar
22	51	2.5	10	22	AAG97007	Human complementar
23	51	2.5	10	22	AAG97009	Human complementar
24	51	2.5	10	22	AAG97011	Human complementar
25	51	2.5	10	22	AAG97013	Human complementar
26	51	2.5	10	22	AAG97017	Human complementar
27	51	2.5	10	22	AAG97031	Human complementar
28	51	2.5	10	22	AAG97033	Human complementar
29	51	2.5	10	22	AAG97041	Human complementar
30	51	2.5	10	22	AAG97049	Human complementar
31	51	2.5	10	22	AAG97051	Human complementar
32	51	2.5	10	22	AAG97053	Human complementar
33	51	2.5	10	22	AAG97055	Human complementar
34	51	2.5	10	22	AAG97069	Human complementar
35	51	2.5	10	22	AAG97071	Human complementar
36	51	2.5	10	22	AAG97073	Human complementar
37	51	2.5	10	22	AAG97075	Human complementar
38	51	2.5	10	22	AAG97077	Human complementar
39	51	2.5	10	22	AAG97079	Human complementar
40	51	2.5	10	22	AAG97085	Human complementar
41	51	2.5	10	22	AAG97093	Human complementar
42	51	2.5	10	22	AAG97095	Human complementar
43	51	2.5	10	22	AAG97097	Human complementar
44	51	2.5	10	22	AAG97105	Human complementar
45	51	2.5	10	22	AAG97107	Human complementar

ALIGNMENTS

RESULT 1
AAR50086
ID AAR50086 standard; Protein; 29 AA.

XX AC AAR50086;

XX DT 25-MAR-2003 (updated)

DT 27-OCT-1994 (first entry)

XX DE Decay accelerating factor derived attachment signal.

XX KW Fusion protein; xenograft; transplantation; membrane; transplamt;

XX KW membrane cofactor protein; MCP; decay accelerating factor; DAF; GPI;

XX KW glycoposphatidyl inositol; anchor; intermembrane transfer.

XX OS Homo sapiens.

XX FH Key

FT Domain

FT Location/Qualifiers

FT 13..29

FT /note= "C-terminal hydrophobic domain."

XX PN WO9406903-A1.

XX PD 31-MAR-1994.

XX PF 22-SEP-1993; 93WO-US08889.

XX PR 22-SEP-1992; 92US-0948521.

XX PA (DNXB-) DNX BIOTHERAPEUTICS INC.

XX PI Byrne GW, Kooyman DL, Logan JS;

XX WPI; 1994-118454/14.
 XX Delivery of proteins, using mobile cell, by intermembrane
 PT transfer - for pre-accommodation of xenogeneic organ transplants
 XX
 XX Disclosure; Page 43; 104pp; English.
 XX
 XX A protein of interest may be delivered to the tissue of a target
 CC animal by providing mobile cells which bear the protein on their
 CC membranes, linked to a glycosphatidyl inositol (GPI) anchor. The
 CC cells circulate in the target animal, coming into contact with the
 CC tissue and transfer the protein to the tissue by intermembrane
 CC transfer. Intermembrane transfer by this method occurs at a greater
 CC rate than naturally in the animal. This sequence is an attachment
 CC signal derived from decay accelerating factor (DAF). DAF is
 CC naturally GPI linked. Preferably, the protein of interest is
 CC expressed as a fusion product, the fusion protein comprising this
 CC sequence and the protein (or fragment) of interest. The method is
 CC especially useful for modifying pig organs for xenotransplantation
 CC into humans. See AAQ58894.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 29 AA;
 SQ
 Query Match 7.1%; Score 147; DB 15; Length 29;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1, 11, 13, 34
 QY 353 SGTRLLSGHTCTLTGLGLTVMGLLT 381
 DB 1 SGTRLLSGHTCTLTGLGLTVMGLLT 29
 RESULT 2
 AAM50805
 ID AAM50805 standard; Peptide; 28 AA.
 XX
 AC AAM50805;
 XX
 DT 01-MAY-2002 (first entry)
 DE Human complement receptor type 1 tryptic peptide 54d.
 XX
 KW Complement receptor type 1; CRI; C3b/C4b receptor; human;
 KW inflammation; myocardial infarction; reperfusion injury;
 KW antiinflammatory; therapy; diagnosis; receptor; purification.
 OS
 OS Homo sapiens.
 XX
 PN US6316604-B1.
 XX
 PD 13-NOV-2001.
 XX
 PF 05-JUN-1995; 95US-0463959.
 XX
 PR 03-APR-1989; 89US-0332865.
 PR 06-DEC-1994; 94US-0350238.
 PR 24-FEB-1993; 93US-0026134.
 PR 01-APR-1988; 88US-0176532.
 XX
 PA (AVAN-) AVANT IMMUNOTHERAPEUTICS INC.
 XX
 PI Fearon DT, Klickstein LB, Wong WW, Carson GR, Concino MF, Ip SH;
 PI Makrides SC, Marsh HC;
 XX
 DR WPI; 2002-121028/16.
 XX
 PT Purifying a recombinant soluble complement receptor type 1 molecule or
 PT its fragment, useful for diagnosing or treating disorders associated
 PT with complement activity, using cation exchange chromatography provides
 PT molecules -
 PT

PS Example; Column 25; 44pp; English.
 XX
 CC The present sequence is that of tryptic peptide 54d of human
 CC erythrocyte C3b/C4b receptor CRI (complement receptor type 1).
 CC The peptide corresponds to amino acids 204-231 and 654-681 of a
 CC full-length CRI sequence (see AAM50797) predicted from isolated cDNA
 CC clones. The invention provides recombinant, soluble CRI polypeptides
 CC that lack the transmembrane domain of the native protein, and methods
 CC of purifying them. CRI polypeptides and nucleic acids have use in
 CC the diagnosis and therapy of disorders involving complement activity
 CC and various immune system or inflammatory disorders. Secreted,
 CC recombinant CRI has been produced in large quantities using CHO host
 CC cells grown in serum-free medium. The purified protein was used to
 CC reduce damage caused by inflammation, and to reduce myocardial
 CC infarct size and prevent reperfusion injury in rats.
 XX
 SQ Sequence 28 AA;
 Query Match 4.3%; Score 89.5; DB 23; Length 28;
 Best Local Similarity 59.3%; Pred. No. 3.9;
 Matches 16; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
 QY 257 FTMIGHSIYCTVNDE-GEWSGPPPE 282
 DB 2 FELVGPSIYCTSDNDQVINGSPAPQ 28
 RESULT 3
 AAW31838
 ID AAW31838 standard; peptide; 23 AA.
 XX
 AC AAW31838;
 XX
 DT 26-MAR-1998 (first entry)
 DE Peptide 4 from the short consensus repeat 3 of complement receptor 1.
 XX
 KW Short consensus repeat 3; long homologous repeat A; LHR-A;
 KW complement receptor 1; CRI; complement inhibition;
 KW anti-haemolytic activity; inflammation; thrombotic condition;
 KW inappropriate complement activation; ARDS; Alzheimer's disease.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9731944-A1.
 XX
 PD 04-SEP-1997.
 XX
 PF 26-FEB-1997; 97WO-BF00994.
 XX
 PR 02-MAR-1996; 96GB-0004518.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Edge CM, Mossakowska DEI, Smith RAG;
 XX
 DR WPI; 1997-448630/41.
 XX
 PT Peptide derived from short consensus repeat 3 of human complement
 PT receptor 1 - between amino acids Cys154-Gly186, useful to treat
 PT disorder or disease associated with inflammation or inappropriate
 PT complement activation
 XX
 PS Claim 13; Page 25; 33pp; English.
 XX
 CC Synthetic soluble peptides AAW31835-38 are derived from the short
 CC consensus repeat 3 of the long homologous repeat A (LHR-A) of human
 CC complement receptor 1 (CRI). The present peptide is located between
 CC residues 164 and 186. These peptides have functional complement
 CC inhibitory, including anti-haemolytic, activity. Enhanced activity
 CC may be achieved by linking the peptides to a core structure
 CC (e.g. the MAP peptide) to produce a multimeric or chimeric polypeptide.

CC This polypeptide can be used to treat a disorder or disease associated
 CC with inflammation or inappropriate complement activation. It can also be
 CC used to treat a thrombotic condition, adult respiratory distress
 CC syndrome (ARDS), wounds, Alzheimer's disease or a CNS inflammatory
 CC disorder, or delay hyperacute allograft or xenograft rejection.
 XX
 SQ Sequence 23 AA;

Query Match 3.1%; Score 64.5; DB 18; Length 23;
 Best Local Similarity 56.5%; Pred. No. 2.6e+02;
 Matches 13; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
 QY 257 FTWIGHSIIYCTVNNDE-GEWSG 278
 Db 1 FELVGEPSIIYSTNDDQVGWSG 23

RESULT 4
 AAG97023
 ID AAG97023 standard; Peptide; 10 AA.

XX AC AAG97023;
 XX XX
 DT 18-SEP-2001 (first entry)
 XX Human complementary peptide, SEQ ID NO: 3217.
 DE Human; complementary peptide; ligand; drug discovery; drug design.
 XX Human; complementary peptide; ligand; drug discovery; drug design.
 XX Homo sapiens.
 OS
 XX WO200142277-A2.
 PN 14-JUN-2001.

XX 13-DEC-2000; 2000WO-GB04776.
 XX 13-DEC-1999; 99GB-0029464.
 PR (PROT-) PROTEOM LTD.
 XX Roberts GW, Heal JR;
 XX WPI; 2001-408419/43.

XX A set of peptide ligands consisting of specific complementary peptides
 PT to proteins encoded by genes of the human genome, useful in an assay
 PT for screening and identifying of one or more novel peptides which are
 PT drug candidates or pro-drugs -
 XX
 PS Example 4; Page 506; 646pp; English.

XX The invention relates to a set of complementary peptide ligands
 CC generated from the human genome. The complementary peptides
 CC interact with their relevant target proteins encoded in the human
 CC genome. They can be used as reagents in drug discovery and as lead
 CC ligands to facilitate drug design and development. The present
 CC sequence is a complementary peptide provided in the specification.
 XX
 SQ Sequence 10 AA;

Query Match 3.0%; Score 61; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 278 GPPPECRGKS 287
 Db 1 GPPPECRGKS 10

RESULT 5
 AAG97081
 ID AAG97081 standard; Peptide; 10 AA.

XX AAG97081;
 AC 18-SEP-2001 (first entry)
 DT Human complementary peptide, SEQ ID NO: 3275.
 DE Human; complementary peptide; ligand; drug discovery; drug design.
 XX Homo sapiens.
 OS WO200142277-A2.
 PN 14-JUN-2001.

XX 13-DEC-2000; 2000WO-GB04776.
 XX 13-DEC-1999; 99GB-0029464.
 PR (PROT-) PROTEOM LTD.
 XX Roberts GW, Heal JR;
 XX WPI; 2001-408419/43.

XX A set of peptide ligands consisting of specific complementary peptides
 PT to proteins encoded by genes of the human genome, useful in an assay
 PT for screening and identifying of one or more novel peptides which are
 PT drug candidates or pro-drugs -
 XX

PS Example 4; Page 514; 646pp; English.

XX The invention relates to a set of complementary peptide ligands
 CC generated from the human genome. The complementary peptides
 CC interact with their relevant target proteins encoded in the human
 CC genome. They can be used as reagents in drug discovery and as lead
 CC ligands to facilitate drug design and development. The present
 CC sequence is a complementary peptide provided in the specification.
 XX

SQ Sequence 10 AA;

Query Match 2.8%; Score 58; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 WSTAVEFCCK 160
 Db 1 WSTAVEFCCK 10

RESULT 6
 AAG97083
 ID AAG97083 standard; Peptide; 10 AA.

XX AAG97083;
 AC 18-SEP-2001 (first entry)
 DT Human complementary peptide, SEQ ID NO: 3277.
 DE Human; complementary peptide; ligand; drug discovery; drug design.
 XX Homo sapiens.
 OS WO200142277-A2.
 PN 14-JUN-2001.

XX 13-DEC-2000; 2000WO-GB04776.
 XX 13-DEC-1999; 99GB-0029464.
 PR (PROT-) PROTEOM LTD.
 XX

KW Human; complementary peptide; ligand; drug discovery; drug design.
 XX Homo sapiens.
 PN WO200142277-A2.
 PD 14-JUN-2001.
 XX 13-DEC-2000; 2000WO-GB04776.
 XX 13-DEC-1999; 99GB-0029464.
 PA (PROT-) PROTEOM LTD.
 XX Roberts GW, Heal JR;
 DR WPI; 2001-408419/43.
 XX A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are drug candidates or pro-drugs -
 XX Example 4; Page 509; 646pp; English.
 PS The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides interact with their relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification.
 XX Sequence 10 AA;
 SQ Query Match 2.7%; Score 55; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 358 LLSGHTCFTL 367
 DB 1 LLSGHTCFTL 10
 RESULT 10
 AAG97089
 ID AAG97089 standard; Peptide; 10 AA.
 AC AAG97089;
 XX 18-SEP-2001 (first entry)
 DE Human complementary peptide, SEQ ID NO: 3283.
 XX Human; complementary peptide; ligand; drug discovery; drug design.
 XX Homo sapiens.
 PN WO200142277-A2.
 PD 14-JUN-2001.
 XX 13-DEC-2000; 2000WO-GB04776.
 XX 13-DEC-1999; 99GB-0029464.
 PA (PROT-) PROTEOM LTD.
 XX Roberts GW, Heal JR;
 DR WPI; 2001-408419/43.
 XX A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay

PT for screening and identifying of one or more novel peptides which are drug candidates or pro-drugs -
 XX Example 4; Page 515; 646pp; English.
 PS The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides interact with their relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification.
 XX Sequence 10 AA;
 SQ Query Match 2.6%; Score 54; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 291 KVPPTVQKPT 300
 DB 1 KVPPTVQKPT 10
 RESULT 11
 AAY65634
 ID AAY65634 standard; Peptide; 19 AA.
 AC AAY65634;
 XX 01-FEB-2000 (first entry)
 DE Oestrogen receptor beta ERE binding peptide 29E-beta.
 XX Oestrogen receptor; estrogen; estradiol; oestrogen response element; ERE; binding; biological activity; fingerprint; molecular braille; cellular braille; modulation; tamoxifen; breast cancer; ovarian cancer; menopause; osteoporosis; selective oestrogen receptor modulator; identification; characterisation; classification.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9954728-A2.
 PN 28-OCT-1999.
 PD 26-MAR-1999; 99WO-US06664.
 XX 23-APR-1998; 98US-0082756.
 PR 09-SEP-1998; 98US-0095656.
 PR 08-JAN-1999; 99US-0115345.
 XX (NOVA-) NOVALON PHARM CORP.
 PA Paige LA, Hamilton PT, Fowlkes DM, Buehrer B, Barnett T;
 PI McDonnell DP, Christensen DJ;
 XX WPI; 2000-013281/01.
 XX Methods for identifying new receptor modulators, especially estrogen modulators to treat tamoxifen refractory breast cancer -
 XX Example 2.2; Page 165; 219pp; English.
 CC The present invention describes a method for predicting the biological activity of new receptor modulating compounds (I) using novel oligomeric peptides (biokeys) which have differential abilities to bind to 2 different receptor conformations. The method is used to identify new drugs that are physiological or pharmacological agonists/antagonists and that target various receptors, which are involved in certain disease conditions. The system may be used as a primary screening tool to identify hits, to classify lead compounds from a drug screen to, characterise selective oestrogen receptor modulators (SERMs) in terms of

agonist and antagonist function and to predict possible clinical effects of SRMs such as tissue and receptor specificity. The method can also be applied to the fractionation of mixtures of SRMs to determine which components are producing agonistic and antagonistic activity. The method may be used with other receptors (e.g. progesterone, dopamine and glucocorticoid, thyroid, vitamin D, beta-adrenergic, androgen, epidermal growth factor, to identify, characterise and classify modulators of receptor activity. Peptides comprising a LXXLL motif may be used to modulate the oestrogen receptor in treating e.g. breast and ovarian cancer and ameliorating the effects of menopause, including osteoporosis. AAY65439 to AAY65652 represent oestrogen receptor, estradiol receptor and oestrogen response element binding peptides given in the exemplification of the present invention. AA235740 to AA235745 represent oligonucleotides used in the exemplification of the present invention.

XX Sequence 19 AA;

Query Match 2.5%; Score 52.5; DB 21; Length 19;
Best Local Similarity 47.6%; Pred. No. 1.7e+03;
Matches 10; Conservative 1; Mismatches 5; Indels 5; Gaps 1;

QY 209 SSVQSDPLPEGREIYCPAPP 229

Db 1 SSYDW-----QCPSWYCPAPP 16

RESULT 12

AAU86371
ID AAU86371 standard; Peptide; 19 AA.

AC AAU86371;

XX 21-MAY-2002 (first entry)

XX Oestrogen receptor beta binding peptide 29E-beta.

DE Oestrogen receptor; breast cancer; combinatorial peptide library;
KW receptor modulating compound.

XX Synthetic.

XX WO200204956-A2.

XX 17-JAN-2002.

XX 11-JUL-2001; 2001WO-US21867.

XX 12-JUL-2000; 2000US-0614865.

XX 21-MAY-2001; 2001US-0860688.

XX (KARO-) KARO BIO USA INC.

XX Fowlkes DM, Barnett TR, Buehrer B;

XX WPI; 2002-154969/20.

XX Identifying receptor-binding peptides comprises screening combinatorial peptide library presented in form of cells each of which coexpress one peptide member and receptor with signal producing system for reporting binding

XX Disclosure; Page 147; 175pp; English.

XX The invention relates to identifying a binding peptide which binds a receptor and which is a member of a combinatorial library of peptides, comprising screening a combinatorial peptide library presented in the form of cells which coexpress the receptor or its ligand-binding receptor moiety and one member of the library, together with a signal producing system for reporting binding of the peptide to the receptor. Also included is a method for predicting the receptor-modulating activity of a compound which modulates the biological activity of a receptor comprising (a) identifying peptides which bind the receptor by the

method above, (b) using a number of the peptides to predict the receptor-modulating activity of a compound by (i) providing a panel of identified peptides, where the members differ in their ability to bind to the receptor depending on reference conformations the receptor is in, where the effect of a number of reference substances known to modulate the biological activity of the receptor on the binding of each member of the panel is known and is characterised as a reference fingerprint for each reference substance, (ii) screening a test substance of unknown activity relative to the receptor to determine its effect on the binding of each member of the panel to the receptor, thereby obtaining a test fingerprint for the test substance, (iii) comparing the test fingerprint to the reference fingerprints and (iv) predicting the biological activity of the test substance based on the assumption that its biological activity will be similar to that of reference substances with similar fingerprints. The method is useful for identifying a binding peptide which binds a vertebrate, mammalian, preferably human receptor, an intracellular, nuclear, oestrogen or androgen receptor. The identified peptides which bind to the receptor are useful for predicting the receptor-modulating activity of a compound (e.g. ant/agonists). The receptor-binding library members are useful in the prediction of the ability of small organic molecules, suitable for pharmaceutical use (e.g. in the case of oestrogen receptors, for breast cancer treatment), to interact with the receptor. The analyte-binding molecules can also be used for in vivo imaging. The method has several advantages over whole animal-based assay systems in that the same technology can be applied to a variety of different receptors, the system can be used for high throughput screening and compound characterisation, and gives very distinct patterns for agonists and antagonists of receptor activity using very much less protein. The present sequence is an oestrogen receptor binding peptide from a combinatorial peptide library.

XX Sequence 19 AA;

Query Match 2.5%; Score 52.5; DB 23; Length 19;

Best Local Similarity 47.6%; Pred. No. 1.7e+03;

Matches 10; Conservative 1; Mismatches 5; Indels 5; Gaps 1;

QY 209 SSVQSDPLPEGREIYCPAPP 229

Db 1 SSYDW-----QCPSWYCPAPP 16

RESULT 13

AAG96997

ID AAG96997 standard; Peptide; 10 AA.

XX AAG96997;

XX 18-SEP-2001 (first entry)

DE Human complementary peptide, SEQ ID NO: 3191.

XX Human; complementary peptide; ligand; drug discovery; drug design.

XX Homo sapiens.

XX WO200142277-A2.

XX 14-JUN-2001.

XX 13-DEC-2000; 2000WO-GB04776.

XX 13-DEC-1999; 99GB-0029464.

XX (PROT-) PROTEOM LTD.

XX Roberts GW, Heal JR;

XX WPI; 2001-408419/43.

XX A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are

PT drug candidates or pro-drugs -

PS Example 4; Page 502; 646pp; English.

XX The invention relates to a set of complementary peptide ligands
CC generated from the human genome. The complementary peptides
CC interact with their relevant target proteins encoded in the human
CC genome. They can be used as reagents in drug discovery and as lead
CC ligands to facilitate drug design and development. The present
CC sequence is a complementary peptide provided in the specification.

XX Sequence 10 AA;

Query Match 2.5%; Score 52; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 196 LFGSTSSFCL 205

Db 1 LFGSTSSFCL 10

RESULT 14

AAG97001

ID AAG97001 standard; Peptide; 10 AA.

XX AAG97001;

XX 18-SEP-2001 (first entry)

XX Human complementary peptide; ligand; drug discovery; drug design.

XX Homo sapiens.

XX WO200142277-A2.

XX 14-JUN-2001.

XX 13-DEC-2000; 2000WO-GB04776.

XX 13-DEC-1999; 99GB-0029464.

XX (PROT-) PROTEOM LTD.

XX Roberts GW, Heal JR;

XX WPI; 2001-408419/43.

XX A set of peptide ligands consisting of specific complementary peptides
XX to proteins encoded by genes of the human genome, useful in an assay
XX for screening and identifying of one or more novel peptides which are
XX drug candidates or pro-drugs -

PS Example 4; Page 503; 646pp; English.

XX The invention relates to a set of complementary peptide ligands
CC generated from the human genome. The complementary peptides
CC interact with their relevant target proteins encoded in the human
CC genome. They can be used as reagents in drug discovery and as lead
CC ligands to facilitate drug design and development. The present
CC sequence is a complementary peptide provided in the specification.

XX Sequence 10 AA;

Query Match 2.5%; Score 52; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 316 TTTKTTTNA 325

Db 1 TTTKTTTNA 10

RESULT 15

AAG97015

ID AAG97015 standard; Peptide; 10 AA.

XX AAG97015;

XX 18-SEP-2001 (first entry)

XX Human complementary peptide; ligand; drug discovery; drug design.

XX Homo sapiens.

XX WO200142277-A2.

XX 14-JUN-2001.

XX 13-DEC-2000; 2000WO-GB04776.

XX 13-DEC-1999; 99GB-0029464.

XX (PROT-) PROTEOM LTD.

XX Roberts GW, Heal JR;

XX WPI; 2001-408419/43.

XX A set of peptide ligands consisting of specific complementary peptides
XX to proteins encoded by genes of the human genome, useful in an assay
XX for screening and identifying of one or more novel peptides which are
XX drug candidates or pro-drugs -

PS Example 4; Page 504; 646pp; English.

XX The invention relates to a set of complementary peptide ligands
CC generated from the human genome. The complementary peptides
CC interact with their relevant target proteins encoded in the human
CC genome. They can be used as reagents in drug discovery and as lead
CC ligands to facilitate drug design and development. The present
CC sequence is a complementary peptide provided in the specification.

XX Sequence 10 AA;

Query Match 2.5%; Score 52; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 192 TGYKLFSGSTS 201

Db 1 TGYKLFSGSTS 10

Search completed: November 18, 2003, 07:43:38

Job time : 50 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2003, 07:42:46 ; Search time 26 Seconds
(without alignments)
1409.241 Million cell updates/sec

Title: US-09-623-035-2

Perfect score: 2064

Sequence: 1 MIVARSPVPAALPLLGELPR.....HTCFTLTGLTGLTVTMGLLT 381

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 6074

Minimum DB seq length: 6

Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*

1: piri:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	2.3	25	2 A48810	fibrinogen B beta
2	41.5	2.0	28	2 I52394	fibronectin, splic
3	40	1.9	26	2 S68302	xanthine dehydrog
4	40	1.9	27	1 TZA23	toxin III - snake-
5	40	1.9	29	2 I78337	copper transportin
6	39	1.9	28	2 I48349	fibronectin - mous
7	38	1.8	24	2 A84023	hypothetical prote
8	38	1.8	26	2 D32248	Ig kappa chain V r
9	38	1.8	26	2 A44036	collagen alpha 1(X
10	38	1.8	27	1 PGFPI	paragonial peptide
11	37.5	1.8	26	2 S65604	sec c 1 protein -
12	37	1.8	11	2 D45900	complement C3b rec
13	37	1.8	20	2 PC1151	tenebrosin 1C - s
14	37	1.8	20	2 B34016	tenebrosin B - sea
15	37	1.8	28	2 B64669	hypothetical prote
16	36.5	1.8	30	2 S59482	hydroxyproline-ric
17	36	1.7	20	2 PC1150	equinotoxin 1B - s
18	36	1.7	26	2 A61195	reverse transcript
19	36	1.7	27	2 PL0029	plasma protein Po2
20	36	1.7	27	2 A84477	5S ribosomal RNA
21	36	1.7	28	2 E49533	T-cell receptor be
22	36	1.7	30	2 A27103	aspartate transami
23	35.5	1.7	29	2 C61384	tracheal mucin gly
24	35	1.7	18	2 JU0125	polypheumusin II -
25	35	1.7	20	2 A34016	tenebrosin A - sea
26	35	1.7	21	2 S08590	NADH2 dehydrogenas
27	35	1.7	24	2 B49480	major immunophilin
28	35	1.7	25	2 I60083	glycophorin A - hu
29	34.5	1.7	20	2 B41299	T-cell receptor al

homeodomain protei
cyclic nucleotide-
glutathione peroxi
173K exoantigen -
Ig heavy chain CDR
30K allergen - rye
u-plasminogen acti
Ig heavy chain DJ
proteoglycan II, b
superoxide dismuta
collagen alpha 1(I
paralytic peptide
paralytic peptide
phycobillissome 29K
neurotoxin III - E

ALIGNMENTS

RESULT 1

A48810
fibrinogen B beta subunit - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: A48810
R:Roberts, L.R.; Nichols, L.A.; Holland, L.J.
Biochemistry 32, 11627-11637, 1993
A:Title: Transcriptional regulation of the Xenopus laevis B beta fibrinogen subunit gene
A:Reference number: A48810; MUID:94032285; PMID:8218230
A:Accession: A48810
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-25 <ROB>
A:Cross-references: GB:U05035; GB:S66373; NID:g450950; PIDN:AAAG0463.1; PID:g450951
A>Note: sequence extracted from NCBI backbone (NCBIN:138880, NCBIP:138881)

Query Match 2.3%; Score 48; DB 2; Length 25;
Best Local Similarity 64.3%; Pred. No. 1.9e+03;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 20 RLLLVLLCLPAVW 33

Db 2 RVLLLPALCVSAW 15

RESULT 2

I52394
fibronectin, splice form II - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C:Accession: I52394; I53217
R:Sekiguchi, K.; Klos, A.M.; Kurachi, K.; Yoshitake, S.; Hakomori, S.
Biochemistry 25, 4936-4941, 1986
A:Title: Human liver fibronectin complementary DNAs: identification of two different mess
A:Reference number: I52394; MUID:87026578; PMID:3021206
A:Accession: I52394
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-28 <RES>
R:Kornblitt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
EMBO J. 3, 221-226, 1984
A:Title: Human fibronectin: Molecular cloning evidence for two mRNA species differing by
A:Reference number: I53217; MUID:84158533; PMID:6200322
A:Accession: I53217
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 3-16 <RE2>
A:Cross-references: GB:K02273; NID:g182698; PIDN:AAA35850.1; PID:g182699
C:Genetics:
A:Gene: GDB:FN1

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178537
copper transporting P-type ATPase - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C/Accession: I78537
R/Thomas, G.R.; Forbes, J.R.; Roberts, E.A.; Walshe, J.M.; Cox, D.W.
Nature Genet. 9, 210-217, 1995
A/Title: The Wilson disease gene: spectrum of mutations and their consequences.
A/Reference number: I58128; MUID:95235569; PMID:7626145
A/Accession: I78537
A/Status: preliminary; translated from GB/EMBL/DBDJ
A/Molecule type: DNA
A/Residues: 1-29 <RES>
A/Cross-references: GB:S77450; NID:g957354; PIDN:AAB34087.1; PID:g957355
C/Genetics:
A/Map position: 13q14.3-13q21.1

Query Match 1.9%; Score 40; DB 2; Length 29;
Best Local Similarity 31.8%; Pred. NO. 8.1e+03;
Matches 7; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 28 CLPAVWGDCGLPPDPVNAQPAL 49
||| : |||
Db 8 CLPSALSEIQFPADIROKSPPL 29

RESULT 6
I48349
fibronectin - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C/Accession: I48349; S33445
R/Polly, P.; Nicholson, R.C.
Gene 137, 353-354, 1993
A/Title: Sequence of the mouse fibronectin-encoding gene promoter region.
A/Reference number: I48349; MUID:94131313; PMID:8299972
A/Accession: I48349
A/Status: preliminary; translated from GB/EMBL/DBDJ
A/Molecule type: DNA
A/Residues: 1-28 <RES>
A/Cross-references: EMBL:Z22729; NID:G297911; PIDN:CAA80422.1; PID:G297912
R/Polly, P.; Nicholson, R.C.
submitted to the EMBL Data Library, May 1993
A/Description: Nucleotide sequence of the murine fibronectin gene promoter region.
A/Reference number: S33445
A/Accession: S33445
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-27 <POL>
A/Cross-references: EMBL:Z22729
C/Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat

Query Match 1.9%; Score 39; DB 2; Length 28;
Best Local Similarity 80.0%; Pred. NO. 9.1e+03;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 20 RLLELLVLLCL 29
||||| :||
Db 9 RLLELLAVLCL 18

RESULT 7
A84023
hypothetical protein BH2985 [imported] - Bacillus halodurans (strain C-125)
C/Species: Bacillus halodurans
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C/Accession: A84023
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiranaka, Y.
Nucleic Acids Res. 28, 4317-4331, 2000
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A/Reference number: A83650; MUID:20512582; PMID:11058132

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Db 2 CEIS

DBb 2 CEETSCDPPP 11

DBb 2 CEETSCDPPP 11

QY 130 RGYRREPSLSPKLTCLQN 148
Db 10 RPPYKFRRLTNKLFQIQS 28

Search completed: November 18, 2003, 07:49:56
Job time : 29 secs

RESULT 13
PC1151
equinatoxin 1C - sea anemone (Actinia equina) (fragment)
C:Species: Actinia equina
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PC1151
R;Komatsu, S.; Furukawa, K.; Abe, K.; Hirano, H.; Ueda, M.
Chem. Pharm. Bull. 40, 2873-2875, 1992
A>Title: Isolation and characterization of equinatoxins from the sea anemone Actinia equina
A/Reference number: PC1149; MUID:93099631; PMID:1361161
A/Accession: PC1151
A/Molecule type: protein
A/Residues: 1-20 <KOM>
C;Keywords: toxin

Query Match 1.8%; Score 37; DB 2; Length 20;
Best Local Similarity 37.5%; Pred. No. 8.5e+03;
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 174 IDVPGGILFGATISFS 189
Db 2 VAVAGAVIEGATLTEN 17

RESULT 14
B34016
tenebrosin B - sea anemone (Actinia tenebrosa) (fragment)
C:Species: Actinia tenebrosa
C/Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 30-Sep-1993
C/Accession: B34016
R;Norton, R.S.; Bobek, G.; Ivanov, J.O.; Thomson, M.; Fiala-Beer, E.; Moritz, R.L.; Simpson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Toxicol 28, 29-41, 1990
A>Title: Purification and characterization of proteins with cardiac stimulatory and haemolytic activity from the sea anemone Actinia tenebrosa
A/Reference number: A34016; MUID:90232538; PMID:1970442
A/Accession: B34016
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-20 <NOR>

Query Match 1.8%; Score 37; DB 2; Length 20;
Best Local Similarity 37.5%; Pred. No. 8.5e+03;
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 174 IDVPGGILFGATISFS 189
Db 2 VAVAGAVIEGATLTEN 17

RESULT 15
B64669
hypothetical protein HP1194 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C/Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C/Accession: B64669
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A>Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A/Reference number: A64520; MUID:97394467; PMID:9252185
A/Accession: B64669
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-28 <TOM>
A/Cross-references: GB:AE000625; GB:AE000511; MID:92314349; PIDN:AAD08244.1; PID:9231435

Query Match 1.8%; Score 37; DB 2; Length 28;
Best Local Similarity 36.8%; Pred. No. 1.2e+04;
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

RESULT 2
US-09-572-404B-3217
; Sequence 3217, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:

```
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3217
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in DAF OR CD55 at 278-287 and may interact with
; OTHER INFORMATION: Sequence 3218 in this patent.
US-09-572-404B-3217

Query Match      3.0%; Score 61; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 GPPPECRGKS 287
Db 1 GPPPECRGKS 10

RESULT 3
US-09-572-404B-3275
; Sequence 3275, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3275
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in DAF OR CD55 at 151-160 and may interact with
; OTHER INFORMATION: Sequence 3276 in this patent.
US-09-572-404B-3275

Query Match      2.8%; Score 58; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 WSTAVEFCCK 160
Db 1 WSTAVEFCCK 10

RESULT 4
US-09-572-404B-3277
; Sequence 3277, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3277
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in DAF OR CD55 at 361-370 and may interact with
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; OTHER INFORMATION: Sequence 3278 in this patent.
US-09-572-404B-3277

Query Match      2.8%; Score 58; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 GHTCFTLTGL 370
Db 1 GHTCFTLTGL 10

RESULT 5
US-09-572-404B-3237
; Sequence 3237, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3237
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in DAF OR CD55 at 123-132 and may interact with
; OTHER INFORMATION: Sequence 3238 in this patent.
US-09-572-404B-3237

Query Match      2.8%; Score 57; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123 TVVEYECRPG 132
Db 1 TVVEYECRPG 10

RESULT 6
US-09-572-404B-3231
; Sequence 3231, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3231
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in DAF OR CD55 at 247-256 and may interact with
; OTHER INFORMATION: Sequence 3232 in this patent.
US-09-572-404B-3231

Query Match      2.7%; Score 55; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 QSVTYACNKG 256
Db 1 QSVTYACNKG 10

RESULT 7
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```
US-09-572-404B-3239
; Sequence 3239, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3239
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in DAF OR CD55 at 358-367 and may interact with
; OTHER INFORMATION: Sequence 3240 in this patent.
US-09-572-404B-3239

Query Match      2.7%; Score 55; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      358 LLSGHTCFTL 367
Db      1 LLSGHTCFTL 10

RESULT 8
US-09-572-404B-3283
; Sequence 3283, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3283
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in DAF OR CD55 at 291-300 and may interact with
; OTHER INFORMATION: Sequence 3284 in this patent.
US-09-572-404B-3283

Query Match      2.6%; Score 54; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      291 KVPPTVQKPT 300
Db      1 KVPPTVQKPT 10

RESULT 9
US-09-572-404B-3191
; Sequence 3191, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3191
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in DAF OR CD55 at 192-201 and may interact with
; OTHER INFORMATION: Sequence 3210 in this patent.
US-09-572-404B-3209
; Sequence 3209, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3209
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in DAF OR CD55 at 192-201 and may interact with
; OTHER INFORMATION: Sequence 3210 in this patent.
US-09-572-404B-3209

Query Match      2.5%; Score 52; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      192 TGYKLFQSTS 201
Db      1 TGYKLFQSTS 201
```

```
US-09-572-404B-3191
; Sequence 3191, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3191
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in DAF OR CD55 at 196-205 and may interact with
; OTHER INFORMATION: Sequence 3192 in this patent.
US-09-572-404B-3191

Query Match      2.5%; Score 52; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      196 LFGSTSSFCL 205
Db      1 LFGSTSSFCL 10

RESULT 10
US-09-572-404B-3195
; Sequence 3195, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3195
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in DAF OR CD55 at 316-325 and may interact with
; OTHER INFORMATION: Sequence 3196 in this patent.
US-09-572-404B-3195

Query Match      2.5%; Score 52; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      316 TTKTKTTPNA 325
Db      1 TTKTKTTPNA 10

RESULT 11
US-09-572-404B-3209
; Sequence 3209, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3209
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in DAF OR CD55 at 192-201 and may interact with
; OTHER INFORMATION: Sequence 3210 in this patent.
US-09-572-404B-3209

Query Match      2.5%; Score 52; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      192 TGYKLFQSTS 201
Db      1 TGYKLFQSTS 201
```

Db 1 TGKLFGSTS 10

RESULT 12

US-09-572-404B-3253
; Sequence 3253, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572,404B

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 4203

; SOFTWARE: ProtPatent version 1.0

; SEQ ID NO 3253

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in DAF OR CD55 at 330-339 and may interact with
; OTHER INFORMATION: Sequence 3254 in this patent.

US-09-572-404B-3253

Query Match 2.5%; Score 52; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 330 STPVSRRTKH 339

Db 1 STPVSRRTKH 10

RESULT 13

US-09-572-404B-3285
; Sequence 3285, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572,404B

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 4203

; SOFTWARE: ProtPatent version 1.0

; SEQ ID NO 3285

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in DAF OR CD55 at 346-355 and may interact with
; OTHER INFORMATION: Sequence 3286 in this patent.

US-09-572-404B-3285

Query Match 2.5%; Score 52; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 NKGGTTSST 355

Db 1 NKGGTTSST 10

RESULT 14

US-09-572-404B-3193
; Sequence 3193, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572,404B

; CURRENT FILING DATE: 2000-05-17

; SOFTWARE: ProtPatent version 1.0

; SEQ ID NO 3193

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in DAF OR CD55 at 348-357 and may interact with
; OTHER INFORMATION: Sequence 3198 in this patent.

; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3193

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in DAF OR CD55 at 348-357 and may interact with
; OTHER INFORMATION: Sequence 3194 in this patent.

US-09-572-404B-3193

Query Match 2.5%; Score 51; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 4.2e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 GSGTTSSTTR 357

Db 1 GSGTTSSTTR 10

RESULT 15

US-09-572-404B-3197
; Sequence 3197, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572,404B

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 4203

; SOFTWARE: ProtPatent version 1.0

; SEQ ID NO 3197

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in DAF OR CD55 at 348-357 and may interact with
; OTHER INFORMATION: Sequence 3198 in this patent.

US-09-572-404B-3197

Query Match 2.5%; Score 51; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 4.2e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 348 GSGTTSSTTR 357

Db 1 GSGTTSSTTR 10

Search completed: November 18, 2003, 07:48:17

Job time : 243 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 18, 2003, 07:42:11 ; Search time 17 Seconds
(without alignments)
1053.951 Million cell updates/sec

Title: US-09-623-035-2

Perfect score: 2064

Sequence: 1 MTVARPSVPAALPLGELPR.....HTCFTLTGLTLVTMGLLT 381

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 1987

Minimum DB seq length: 6

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	1.9	27	1 TXA3 ANESU	P01535 anemonia su
2	39.5	1.9	23	1 NEU_LITCE	P01872 litoria cae
3	38	1.8	27	1 PPS1 DROFU	P01372 drosophila
4	37	1.8	20	1 TENB ACTTE	P30834 actinia ten
5	37	1.8	25	1 SODC PAROL	P81129 paralichthy
6	36.5	1.8	27	1 CX2B CONBE	P81727 conus betul
7	36	1.7	21	1 JAP2_RANJA	P83306 rana japoni
8	36	1.7	23	1 CP23_SPOER	P56683 spodoptera
9	36	1.7	30	1 AATC RABIT	P12343 oryctolagus
10	36	1.7	30	1 TAT HVIZH	P12512 human immu
11	35	1.7	18	1 PPM2 LIMPO	P14216 limulus pol
12	35	1.7	20	1 TENA ACTTE	P30833 actinia ten
13	34.5	1.7	28	1 SLPI_LEIQH	P80669 leirus qui
14	34	1.6	23	1 PAPI_SPOEX	P30255 spodoptera
15	34	1.6	23	1 PAP2_SPOEX	P30256 spodoptera
16	34	1.6	23	1 PAP3_SPOEX	P30257 spodoptera
17	34	1.6	28	1 NXLI_BOUAN	P34074 bouleangerin
18	33.5	1.6	13	1 BPPI_BOTJA	P31020 bothrops ja
19	33.5	1.6	23	1 SCK1_TITCA	P83243 titiys camb
20	33.5	1.6	30	1 VARG_VIOAR	P58452 viola arven
21	33	1.6	25	1 AUIS_LITRA	P82401 litoria ran
22	33	1.6	29	1 VARE_VIOAR	P58451 viola arven
23	33	1.6	30	1 VARE_VIOAR	P58447 viola arven
24	32.5	1.6	26	1 CXO6_CONTU	P58915 conus tulip
25	32.5	1.6	26	1 NIFQ_ENTAG	P28580 enterobacte
26	32.5	1.6	27	1 ACH4_MOUSE	O70174 mus musculu
27	32.5	1.6	28	1 SCX2_BUTSI	P15230 buthus sind
28	32	1.6	12	1 CD11_LITXA	P56245 litoria xan
29	32	1.6	16	1 CXAA_CONPE	P50984 conus penna
30	32	1.6	18	1 PPM1_LIMPO	P14215 limulus pol
31	32	1.6	21	1 GYRA_STRSH	P50071 streptomyc
32	32	1.6	22	1 LANM_STRMU	P80666 streptococ
33	32	1.6	23	1 ALL5_HORSE	P82616 equus cabal

ALIGNMENTS

RESULT 1
TXA3_ANESU
ID TXA3_ANESU STANDARD; PRT; 27 AA.
AC P01535;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurotoxin III (Toxin ATX-III)
OS Anemonia sulcata (Snake-locks sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anemonia.
OX NCBI_TaxID=6108;
RN [1]
RP SEQUENCE.
RC TISSUE=Cnidoblast;
RX MEDLINE=78084776; PubMed=23311;
RA Martinez G., Kopeyan C., Schweitz H., Lazdunski M.;
RT "Toxin III from Anemonia sulcata: primary structure.";
RL FEBS Lett. 84:247-252 (1977).
RN [2]
RP PRELIMINARY SEQUENCE.
RX MEDLINE=78044787; PubMed=21843;
RA Beress L., Wunderer G., Wachter E.;
RT "Amino acid sequence of toxin III from Anemonia sulcata.";
RN [3]
RP Hoppe-Seyler's Z. Physiol. Chem. 358:985-988 (1977).
RN [4]
RP STRUCTURE BY NMR.
RX MEDLINE=93343891; PubMed=8102051;
RA Norton R.S., Cross K., Braach-Maksvytis V., Wachter E.;
RT "1H-NMR study of the solution properties and secondary structure of neurotoxin III from the sea anemone Anemonia sulcata.";
RL Biochem. J. 293:545-551 (1993).
RN [5]
RP STRUCTURE BY NMR.
RX MEDLINE=95244415; PubMed=7727358;
RA Manoleras N., Norton R.S.;
RT "Three-dimensional structure in solution of neurotoxin III from the sea anemone Anemonia sulcata.";
RL Biochemistry 33:11051-11061 (1994).
CC -1- FUNCTION: BINDS SPECIFICALLY TO THE SODIUM CHANNEL.
CC -1- SUBCELLULAR LOCATION: Secreted; cnidocyst.
CC -1- SIMILARITY: BELONGS TO THE SEA ANEMONE SHORT TOXIN FAMILY.
DR PIR; A91446; T2A23.
DR PDB; 1ANS; 31-AUG-94.
KW Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor;
FT DISULFID 3 17
FT DISULFID 4 11
FT DISULFID 6 22
FT CONFLICT 22 23 CS -> SC (IN REF. 2).
FT TURN 7 10
SQ SEQUENCE 27 AA; 2938 MW; AA4E261FFAF34A7A CRC64;
Query Match 1.9%; Score 40; DB 1; Length 27;
Best Local Similarity 26.7%; Pred. No. 3.5e+03;
Matches 8; Conservative 2; Mismatches 8; Indels 12; Gaps 1;

P24160 conus texti
P09355 apis mellif
P81798 echis multi
P58783 conus ermin
P04097 buthus occi
P31083 synechococ
P82230 viola odora
P80936 arachis hyp
P27459 achromobact
P16852 triticum ae
P83447 pseudananas
P11419 desulfovibr

34 32 1.6 27 1 CX7A CONTE
35 32 1.6 27 1 LSP APIME
36 32 1.6 29 1 MULR ECHML
37 32 1.6 30 1 CXVB CONER
38 31.5 1.5 24 1 SCX5 BUTOC
39 31.5 1.5 29 1 PSAP_SNP6
40 31.5 1.5 30 1 CYO1_VIOOD
41 31 1.5 24 1 CS33 ARAHY
42 31 1.5 25 1 PRLA ACHLY
43 31 1.5 27 1 IAI7 WHEAT
44 31 1.5 27 1 MDO2_PSEMR
45 31 1.5 27 1 SODM_DESDE

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QY 28 CLPAVWDCGLPDPVFNPAQALSGRTSPFE 57
DB 3 CCPCYMGCCPW-----GQNCYPE 20

RESULT 2
NEUU_LITCE STANDARD; PRT; 23 AA.
AC P81872;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neuromedin U-23 (NMU-23).
OS Litoria caerulea (Green tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=30344;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Skin secretion;
RX MEDLINE=20138182; PubMed=10671478;
RA Salmon A.L., Johnsen A.H., Bienert M., McMurray G., Nandha K.A.,
RA Bloom S.R., Shaw C.;
RT "Isolation, structural characterization and bioactivity of a novel
RT neuromedin U analog from the defensive skin secretion of the
RT Australasian tree frog Litoria caerulea."
RL J. Biol. Chem. 275:4549-4554(2000).
CC -I- FUNCTION: STIMULATE UTERINE SMOOTH MUSCLE CONTRACTION AND CAUSE
CC SELECTIVE VASOCONSTRICTION.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Skin.
CC -I- SIMILARITY: BELONGS TO THE NMU FAMILY.
DR InterPro: IPR001942; NMU.
DR Pfam: PF02070; NMU; 1.
DR PROSITE: PS00967; NMU; 1.
KW Amidation; Hormone.
FT MOD RES 23 23 AMIDATION.
SQ SEQUENCE 23 AA; 2581 MW; A94958415CB58DC3 CRC64;

Query Match 1.9%; Score 39.5; DB 1; Length 23;
Best Local Similarity 32.0%; Pred. No. 3.2e+03;
Matches 8; Conservative 5; Mismatches 3; Indels 9; Gaps 1;

QY 173 QIDVPGGILFGATISFCNTGYKLF 197
DB 4 EVQVPGGVI-----SNGYFLF 19

RESULT 3
PPSI_DROFU STANDARD; PRT; 27 AA.
AC P01372;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Paragonial peptide P5-1 (Paragonial peptide C).
GN PAPC.
OS Drosophila funebris (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7221;
RN [1]
RP SEQUENCE.
RX MEDLINE=77245908; PubMed=1236144;
RA Baumann H., Wilson K.J., Chen P.S., Humbel R.E.;
RT "The amino-acid sequence of a peptide (PS-1) from Drosophila
RT funebris: a paragonial peptide from males which reduces the
RT receptivity of the female."
RL Eur. J. Biochem. 52:521-529(1975).
CC -I- FUNCTION: REPRESSIONS FEMALE SEXUAL RECEPTIVITY AND STIMULATES
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CC OVIPOSITION. THIS PEPTIDE HAS A LOW ACTIVITY.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: MAIN CELLS OF THE ACCESSORY GLANDS OF MALES
CC (PARAGONIAL GLAND).
DR PIR; A01643; PGFF1.
DR FlyBase; FBgn0004112; Dfun\PapC.
KW Behavior.
FT VARIANT 2 2 V -> L (IN 30% OF THE MOLECULES).
SQ SEQUENCE 27 AA; 2669 MW; D8083427974AD5D6 CRC64;

Query Match 1.8%; Score 38; DB 1; Length 27;
Best Local Similarity 26.9%; Pred. No. 4.8e+03;
Matches 7; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 303 NYPTEVSPTSOKTTTKTTTPNAQAT 328
DB 1 DVPSANANANNQRTAAAKPQANAAS 26

RESULT 4
TENB_ACTTE STANDARD; PRT; 20 AA.
AC P30834;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tenebrosin B (Fragment).
OS Actinia tenebrosa (Australian red waratah sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Actinia.
OX NCBI_TaxID=6105;
RN [1]
RP SEQUENCE.
RX MEDLINE=90232538; PubMed=1970442;
RA Norton R.S., Bobek G., Ivanov J.O., Thomson M., Fiala-Beer E.,
RA Moritz R.L., Simpson R.J.;
RT "Purification and characterisation of proteins with cardiac
RT stimulatory and haemolytic activity from the anemone Actinia
RT tenebrosa."
RL Toxicol 28:29-41(1990).
CC -I- FUNCTION: This cardiac stimulatory and hemolytic protein is a
CC channel-forming and/or membrane-penetrating protein.
CC -I- SUBCELLULAR LOCATION: Secreted; Cnidocyst.
CC -I- SIMILARITY: BELONGS TO THE TENEBROSIN FAMILY.
DR PIR; B34016; B34016.
DR Cytolysis; Hemolysis; Toxin; Cnidocyst; Transmembrane.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 1960 MW; FA32B426009FF5FA CRC64;

Query Match 1.8%; Score 37; DB 1; Length 20;
Best Local Similarity 37.5%; Pred. No. 4.1e+03;
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 174 IDVPGGILFGATISFS 189
DB 2 VAVAGAVIEGALTFFN 17

RESULT 5
SODC_PAROL STANDARD; PRT; 25 AA.
AC P83129;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Cu-Zn] (EC 1.15.1.1) (Fragment).
OS Paralichthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralichthyidae; Paralichthys.
OX NCBI_TaxID=8255;
RN [1]
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SEQUENCE, AND CHARACTERIZATION.
RC TISSUE=Hepatopancreas;
RX MEDLINE=21186415; PubMed=11290457;
RA Osatomi K., Masuda Y., Hara K., Iehihara T.;
RT "Purification, N-terminal amino acid sequence, and some properties of
RT Cu, Zn-superoxide dismutase from Japanese flounder (Paralichthys
RT olivaceus) hepato-pancreas.";
RL Comp. Biochem. Physiol. 128B:751-760(2001).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems (By similarity).
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
CC similarity).
CC -!- SUBUNIT: Homotrimer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE
CC FAMILY.
DR GO: GO:0005737; Cytoplasm; TAS.
DR GO: GO:0005507; F: copper ion binding activity; ISS.
DR GO: GO:0004785; F: copper, zinc superoxide dismutase activity; IDA.
DR GO: GO:0008270; F: zinc ion binding activity; ISS.
DR GO: GO:0019430; P: removal of superoxide radicals; TAS.
DR InterPro: IPR001424; SOD_CU_ZN.
DR Pfam: PF00800; sodcu; 1.
DR PROSITE: PS00087; SOD_CU_ZN_1; PARTIAL.
DR PROSITE: PS00332; SOD_CU_ZN_2; PARTIAL.
KW Antioxidant; Oxidoreductase; Metal-binding; Copper; Zinc.
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2604 MW; 76C4321D740857C5 CRC64;

Query Match 1.8%; Score 37; DB 1; Length 25;
Best Local Similarity 77.8%; Pred. No. 5.2e+03;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 347 KCSGTSST 355
DB 9 KGAGTSST 17
||:|||||

RESULT 6
CX2B_CONBE STANDARD; PRT; 27 AA.
AC P81727;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Conotoxin BcXIIb.
OS Conus betulinus (Beech cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89764;
[1]
RN SEQUENCE, MASS SPECTROMETRY, AND HYDROXYLATION.
RC TISSUE=Venom;
RX MEDLINE=20058566; PubMed=10591037;
RA Chen J.-S., Fan C.-X., Hu K.-P., Wei K.-H., Zhong M.-N.;
RT "Studies on conotoxins of Conus betulinus.";
RL J. Nat. Toxins 8:341-349(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=2664.3; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE P-SUPERFAMILY OF CONOTOXINS.
KW Neurotoxin; Toxin; Hydroxylation.
FT DISULFID 2 16 BY SIMILARITY.
FT DISULFID 6 19 BY SIMILARITY.
FT DISULFID 12 24 BY SIMILARITY.
FT MOD_RES 13 13 HYDROXYLATION.
SQ SEQUENCE 27 AA; 2651 MW; 60F0500514C7F1BA CRC64;

Query Match 1.8%; Score 36.5; DB 1; Length 27;
Best Local Similarity 44.4%; Pred. No. 6.1e+03;
Matches 8; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

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QY 178 GGI-LFGATISPSCNTGY 194
DB 3 GGVCAYGSCPPSCNTCY 20
||:|||||

RESULT 7
JAP2_RANJA STANDARD; PRT; 21 AA.
ID JAP2_RANJA STANDARD; PRT; 21 AA.
AC P83306;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Japonicin-2.
OS Rana japonica (Japanese reddish frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8402;
[1]
RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RP TISSUE=Skin secretion;
RX MEDLINE=21826910; PubMed=11835990;
RA Isaacson T., Soto A., Iwamuro S., Knoop F.C., Conlon J.M.;
RT "Antimicrobial peptides with atypical structural features from the
RT skin of the Japanese brown frog Rana japonica.";
RL Peptides 23:419-425(2002).
CC -!- FUNCTION: Antibacterial activity against the Gram-negative
CC bacterium E.coli and the Gram-positive bacterium S.aureus.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=2685.4; METHOD=Electrospray.
KW Amphibian defense peptide; Antibiotic.
FT DISULFID 14 21 BY SIMILARITY.
SQ SEQUENCE 21 AA; 2358 MW; AB055DF897566BDF CRC64;

Query Match 1.7%; Score 36; DB 1; Length 21;
Best Local Similarity 46.7%; Pred. No. 5e+03;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 12 LPLGLPRLLLVL 26
DB 3 LPLSLPKALCILL 17
||:|||||

RESULT 8
CP23_SPOER STANDARD; PRT; 23 AA.
ID CP23_SPOER STANDARD; PRT; 23 AA.
AC P56683;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cardioactive peptide CAP23.
OS Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Amphipyrae; Spodoptera.
OX NCBI_TaxID=37547;
[1]
RN SEQUENCE.
RP MEDLINE=99196260; PubMed=10098624;
RX Furiya K., Hackett M., Cirelli M.A., Schegg K.M., Wang H.,
RA Shabanowitz J., Hunt D.F., Schooley D.A.;
RT "A cardioactive peptide from the southern armyworm, Spodoptera
RT eridania.";
RL Peptides 20:53-61(1999).
CC -!- FUNCTION: HAS EXCITATORY EFFECTS ON A SEMI-ISOLATED HEART FROM
CC LARVAL MANDUCA SEXTA, CAUSING AN INOTROPIC EFFECT AT LOW
CC CONCENTRATIONS OF PEPTIDE AND CHRONOTROPIC AND INOTROPIC EFFECTS
CC AT HIGH DOSES.
CC -!- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
DR HSSP; 061704; 1B1V.
DR InterPro: IPR003463; GBP_PSP.
DR Pfam: PF02425; GBP_PSP; 1.

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DR ProDom: PD006507; GBP_PSP: 1. BY SIMILARITY.
FT DISULFID 7 19
SQ SEQUENCE 23 AA; 2519 MW; 0A96D72A70855AE0 CRC64;

Query Match 1.7%; Score 36; DB 1; Length 23;
Best Local Similarity 47.1%; Pred. No. 5.5e+03;
Matches 8; Conservative 1; Mismatches 2; Indels 6; Gaps 1;

QY 119 FPGVTVEECRPGYR 135
DB 3 FAVG-----CTPGYR 13

RESULT 9
AATC_RABIT STANDARD; PRT; 30 AA.
AC P12343;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Aspartate aminotransferase, cytoplasmic (EC 2.6.1.1) (Transaminase A)
DE Glutamate oxaloacetate transaminase-1 (Fragment).
GN GOT1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=85289123; PubMed=4030726;
RA Kuramitsu S., Inoue K., Kondo K., Aki K., Kagamiyama H.;
RT "Aspartate aminotransferase isozymes from rabbit liver. Purification
and properties.";
RL J. Biochem. 97:1337-1345(1985).
CC -!- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +
L-glutamate.
CC -!- COFACTOR: Pyridoxal phosphate.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: In eukaryotes there are cytoplasmic, mitochondrial
and chloroplastic isozymes.
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
AMINOTRANSFERASES.
CC PIR; A27103; A27103.
DR HSSP; P00503; 1AJS.
DR InterPro; IPR004838; NHTransf 1.
DR PROSITE; PS00105; AA_TRANSFER_CLASS 1; PARTIAL.
KW Transferase; Aminotransferase; Pyridoxal phosphate.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3296 MW; 9B76CEEAC2FC5D98 CRC64;

Query Match 1.7%; Score 36; DB 1; Length 30;
Best Local Similarity 42.3%; Pred. No. 7.4e+03;
Matches 11; Conservative 2; Mismatches 7; Indels 6; Gaps 2;

QY 39 PP-----DVNPAQALGR--TSPED 58
DB 2 PPSIFAEVPAQPVLFKLTADPRD 27

RESULT 10
TAT_HV12H STANDARD; PRT; 30 AA.
AC P12512;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TAT protein (transactivating regulatory protein) (Fragment).
GN TAT.
OS Human immunodeficiency virus type 1 (Zaire HZ321 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11692;

[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=89228766; PubMed=2713163;
RA Srinivasan A., York D., Butler D. Jr., Jannoun-Nasr R., Getchell-J.,
RA McCormick J., Ou C.Y., Myers G., Smith T., Chen E.;
RT "Molecular characterization of HIV-1 isolated from a serum collected
in 1976: nucleotide sequence comparison to recent isolates and
generation of hybrid HIV.";
RL AIDS Res. Hum. Retroviruses 5:121-129(1989).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC EMBL; M15896; AAB53949.1; -
DR HIV; M15896; TAT52321.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
FT NON_TER 1 1
SQ SEQUENCE 30 AA; 3329 MW; 545F848858040A1F CRC64;

Query Match 1.7%; Score 36; DB 1; Length 30;
Best Local Similarity 43.8%; Pred. No. 7.4e+03;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 304 VPTTEVSPTSQKTTK 319
DB 2 LPTTRGNPTGPKESK 17

RESULT 11
PPM2_LIMPO STANDARD; PRT; 18 AA.
ID P14216;
AC P14216;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Polyphephusin II.
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Limulus.
OX NCBI_TaxID=6850;
RN [1]
RP SEQUENCE.
RA MEDLINE=90110066; PubMed=2514185;
RA Miyata T., Tokunaga F., Yonaga T., Yoshikawa K., Iwanaga S., Niwa M.,
RA Takao T., Shimonishi Y.;
RT "Antimicrobial peptides, isolated from horseshoe crab hemocytes,
and tachyplesin II, and polyphephusins I and II: chemical structures and
biological activity.";
RL J. Biochem. 106:663-668(1989).
CC -!- FUNCTION: SIGNIFICANTLY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND
GRAM-POSITIVE BACTERIA.
CC -!- TISSUE SPECIFICITY: HEMOCYTES.
CC -!- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEPHUSIN FAMILY.
DR PIR; JU0125; JU0125.
KW Antibiotic; Amidation.
FT DISULFID 4 17 BY SIMILARITY.
FT DISULFID 8 13 BY SIMILARITY.
FT MOD_RES 18 18 AMIDATION.
SQ SEQUENCE 18 AA; 2431 MW; E402A109D2923504 CRC64;

Query Match 1.7%; Score 35; DB 1; Length 18;

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Best Local Similarity 36.8%; Pred. No. 5e+03;
Matches 7; Conservative 1; Mismatches 3; Indels 8; Gaps 1;

QY 80 ICLGQSDIEFCNRS 98
: : : : :
7 VCYKG-----FCYRK 17

Db

RESULT 12
TENA ACTTE STANDARD; PRT; 20 AA.
AC P30833;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tenebrosin A (Fragment).
OS Actinia tenebrosa (Australian red waratah sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Actinia.
OX NCBI_TaxID=6105;
RN [1]
RP SEQUENCE.
RX MEDLINE=90232538; PubMed=1970442;
RA Norton R.S., Bobek G., Ivanov J.O., Thomson M., Fiala-Beer E.,
RA Moritz R.L., Simpson R.J.;
RT "Purification and characterisation of proteins with cardiac
RT stimulatory and haemolytic activity from the anemone Actinia
RT tenebrosa".
RL Toxicon 28:29-41(1990).
CC -!- FUNCTION: This cardiac stimulatory and hemolytic protein is a
CC channel-forming and/or membrane-penetrating protein.
CC -!- SUBCELLULAR LOCATION: Secreted; chnidoctyst.
CC -!- SIMILARITY: BELONGS TO THE TENEBROSIN FAMILY.
DR PIR; A34016; A34016.
KW Cytolysis; Hemolysis; Toxin; Chnidoctyst; Transmembrane.
FT NON_TER 20
SQ SEQUENCE 20 AA; 1974 MW; F32AC8BDAAPF5FA CRC64;

Query Match 1.7%; Score 35; DB 1; Length 20;
Best Local Similarity 46.2%; Pred. No. 5.6e+03;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 176 VPGGILFGATISF 188
: : : : :
4 VAGAVIEGATLTF 16

Db

RESULT 13
SLPI LEIQH STANDARD; PRT; 28 AA.
AC P80669;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leuropeptide I.
OS Leiurus quinquestriatus hebraeus (Yellow scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Leiurus.
OX NCBI_TaxID=6884;
RN [1]
RP SEQUENCE, AND STRUCTURE BY NMR.
RC TISSUE=Venom;
RX MEDLINE=97411504; PubMed=9266482;
RA Buissine E., Wieruzecki J.-M., Lippens G., Wouters D., Tartar A.,
RA Sautiere P.;
RT venom of the scorpion Leiurus quinquestriatus hebraeus from the
RT structure of leuropeptide II.";
RL J. Pept. Res. 49:545-555(1997).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: BELONGS TO THE SCORPION LEIUROTOXIN FAMILY.
DR HSSP; Q9NJPF; 1DU9.

KW Toxin.
FT DISULFID 3 19
FT DISULFID 6 24
FT DISULFID 10 26
SQ SEQUENCE 28 AA; 2954 MW; 5F72AD78BD39BE1B CRC64;

Query Match 1.7%; Score 34.5; DB 1; Length 28;
Best Local Similarity 39.1%; Pred. No. 8.7e+03;
Matches 9; Conservative 1; Mismatches 4; Indels 9; Gaps 2;

QY 220 CREIYCP-----APQIDNGI 235
: : : : :
3 CEE--CPMECKGKNAKPTCDNGV 23

Db

RESULT 14
PAP1 SPOEX STANDARD; PRT; 23 AA.
ID _PAP1_SPOEX
AC P30255;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Paralytic peptide I (pp I).
OS Spodoptera exigua (Beet armyworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Noctuoidea;
OC Noctuidae; Amphipyrrinae; Spodoptera.
OX NCBI_TaxID=7107;
RN [1]
RP SEQUENCE.
RX TISSUE=Hemolymph;
RX MEDLINE=91302298; PubMed=2071576;
RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
RA Quistad G.B.;
RT "Isolation and identification of paralytic peptides from hemolymph of
RT the lepidopteran insects Manduca sexta, Spodoptera exigua, and
RT Heliothis virescens".
RL J. Biol. Chem. 266:12873-12877(1991).
CC -!- FUNCTION: CAUSES RAPID, RIGID, PARALYSIS WHEN INJECTED INTO
CC LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
CC HEMOLYPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
CC -!- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
DR PIR; C39855; C39855.
DR HSSP; O61704; 1B1V.
DR InterPro; IPR003463; GBP_PSP.
DR Pfam; PF02425; GBP_PSP; 1.
DR ProDom; PD006507; GBP_PSP; 1.
KW Hemolymph.
FT DISULFID 7 19
SQ SEQUENCE 23 AA; 2451 MW; 0A96D1F600855AE0 CRC64;

Query Match 1.6%; Score 34; DB 1; Length 23;
Best Local Similarity 71.4%; Pred. No. 7.6e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 129 CRPGYRR 135
: : : : :
7 CTPGYQR 13

Db

RESULT 15
PAP2 SPOEX STANDARD; PRT; 23 AA.
ID _PAP2_SPOEX
AC P30256;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Paralytic peptide II (pp II).
OS Spodoptera exigua (Beet armyworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Noctuoidea;
OC Noctuidae; Amphipyrrinae; Spodoptera.
OX NCBI_TaxID=7107;

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RN [1]
RP SEQUENCE
RC TISSUE=Hemolymph; PubMed=2071576;
RX MEDLINE=91302298; Li J.P., Summerfelt R.M., Carney R.L.,
RA Skinner W.S., Dennis P.A., Quistad G.B.;
RT "Isolation and identification of paralytic peptides from hemolymph of
RT the lepidopteran insects Manduca sexta, Spodoptera exigua, and
RT Heliothis virescens."
RL J. Biol. Chem. 266:12873-12877(1991).
CC -1- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
CC LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
CC HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
CC -1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
DR PIR; D39855; D39855.
DR HSP; O61704; IB1V.
DR InterPro; IPR003463; GBP_PSP.
DR Pfam; PF02425; GBP_PSP; 1.
DR ProDom; PD006507; GBP_PSP; 1.
KW Hemolymph.
FT DISULFID 7 19 BY SIMILARITY.
SQ SEQUENCE 23 AA; 2477 MW; 0A96CB460085BAE0 CRC64;

Query Match 1.6%; Score 34; DB 1; Length 23;
Best Local Similarity 71.4%; Pred. No. 7.6e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 129 CRFGYRR 135
Db | | | | |
7 CTGYQR 13
```

Search completed: November 18, 2003, 07:42:42
Job time : 19 secs

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OM protein - protein search, using sw model

Run on: November 18, 2003, 07:42:16 ; Search time 56 Seconds
(without alignments)
1755.679 Million cell updates/sec

Title: US-09-623-035-2
Perfect score: 2064
Sequence: 1 MVARPSVPAALPLLGELPR.....HTCFTLTGLLTVMGLLT 381

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 16438

Minimum DB seq length: 6
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriaph:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	2.3	30	5 Q27545	Q27545 crithidia f
2	45.5	2.2	25	6 Q98G19	Q98G19 cheirogaleu
3	44.5	2.2	22	11 Q9RIC1	Q9RIC1 mus musculu
4	43	2.1	29	15 Q71992	Q71992 human endog
5	40.5	2.0	20	4 Q96T45	Q96T45 homo sapien
6	40.5	2.0	26	11 Q9JMC5	Q9JMC5 rattus norv
7	40.5	2.0	30	11 Q9QV95	Q9QV95 cavia (guin
8	40	1.9	20	3 Q9URC1	Q9URC1 phanerochae
9	40	1.9	27	13 Q57555	Q57555 lampetra pl
10	40	1.9	27	13 Q57554	Q57554 lampetra pl
11	40	1.9	30	11 Q9JK06	Q9JK06 mus musculu
12	39.5	1.9	26	5 Q8N066	Q8N066 plasmodium
13	39	1.9	25	6 Q9BGJ0	Q9BGJ0 eulemur mac
14	39	1.9	27	12 Q9IJ66	Q9IJ66 hepatitis c
15	39	1.9	28	6 Q9XS67	Q9XS67 bos taurus
16	39	1.9	30	13 Q9PRP7	Q9PRP7 echis carin

17	38.5	1.9	30	13 Q9PRP8	Q9PRP8 echis carin
18	38	1.8	19	6 Q8MJ41	Q8MJ41 bos taurus
19	38	1.8	23	11 Q64014	Q64014 mus sp. inh
20	38	1.8	23	11 Q9R231	Q9R231 rattus norv
21	38	1.8	24	16 Q9K8M1	Q9K8M1 bacillus ha
22	38	1.8	25	12 Q11469	Q11469 hepatitis c
23	38	1.8	26	6 Q9TRM6	Q9TRM6 bos taurus
24	38	1.8	27	5 Q23745	Q23745 ctenodrilus
25	38	1.8	30	4 Q96D69	Q96D69 homo sapien
26	37.5	1.8	25	2 Q07916	Q07916 mycobacteri
27	37.5	1.8	26	10 Q9S8H2	Q9S8H2 secale cere
28	37.5	1.8	27	12 Q9QIB5	Q9QIB5 hepatitis c
29	37.5	1.8	27	12 Q9QIC1	Q9QIC1 hepatitis c
30	37.5	1.8	27	12 Q9QIB3	Q9QIB3 hepatitis c
31	37.5	1.8	27	12 Q9QIB9	Q9QIB9 hepatitis c
32	37.5	1.8	27	12 Q9QIB2	Q9QIB2 hepatitis c
33	37.5	1.8	27	12 Q9QIC7	Q9QIC7 hepatitis c
34	37.5	1.8	27	12 Q9QIB6	Q9QIB6 hepatitis c
35	37.5	1.8	27	12 Q9QIC6	Q9QIC6 hepatitis c
36	37.5	1.8	27	12 Q9QIB0	Q9QIB0 hepatitis c
37	37.5	1.8	27	12 Q9QIB4	Q9QIB4 hepatitis c
38	37.5	1.8	27	12 Q9QIC4	Q9QIC4 hepatitis c
39	37.5	1.8	27	12 Q9QIB7	Q9QIB7 hepatitis c
40	37.5	1.8	27	12 Q9QIC0	Q9QIC0 hepatitis c
41	37.5	1.8	27	12 Q9QIC9	Q9QIC9 hepatitis c
42	37.5	1.8	27	12 Q9QIB8	Q9QIB8 hepatitis c
43	37.5	1.8	27	12 Q9QIC5	Q9QIC5 hepatitis c
44	37.5	1.8	30	12 Q9QS21	Q9QS21 hepatitis b
45	37.5	1.8	30	12 Q9QS15	Q9QS15 hepatitis b

ALIGNMENTS

RESULT 1

Q27545 PRELIMINARY; PRT; 30 AA.
AC Q27545;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Reiske iron-sulfur protein precursor (EC 1.10.2.2) (Fragment).
OS Crithidia fasciculata.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Crithidia.
OX NCBI_TaxID=5656;
RN [1]_TaxID=5656;
RP SEQUENCE FROM N.A.
RX MEDLINE=96096683; PubMed=7495871;
RA Priest J.W., Hajduk S.L.;
RT "The trypanosomatid Reiske iron-sulfur proteins have a cleaved presequence that may direct mitochondrial import.";
RL Biochim. Biophys. Acta 1269:201-204(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93015890; PubMed=1328195;
RA Priest J.W., Hajduk S.L.;
RT "Cytochrome c reductase purified from Crithidia fasciculata contains an atypical cytochrome c1.";
RL J. Biol. Chem. 267:20188-20195(1992).
KW Mitochondrion; Oxidoreductase; Transit peptide.
FT TRANSIT 1 17 MITOCHONDRION.
FT CHAIN 18 >30 REISKE IRON-SULFUR PROTEIN.
FT NON-TER 30 30
SQ SEQUENCE 30 AA; 3399 MW; DE41365941814501 CRC64;

Query Match 2.3%; Score 48; DB 5; Length 30;

Best Local Similarity 44.4%; Pred. No. 2.2e+03;

Matches 12; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 319 KTTTNAQATRTPTVSRRTTKFHETTP 345

Db 4 RTFTTAFQATRAARVSLVKKLEGTTP 30

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RESULT 2
Q9BG19 ID Q9BG19 PRELIMINARY; PRT; 25 AA.
AC Q9BG19;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DE ATP synthase beta subunit (Fragment).
OS Cheirogaleus medius (Fat-tailed dwarf lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;
OC Cheirogaleus.
OX NCBI_TaxID=9460;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21100352; PubMed=11156996;
RA Schmitz J., Ohme M., Zischler H.;
RT "SINE Insertions in Cladistic Analyses and the Phylogenetic
RT Affiliations of Tarsius bancanus to Other Primates.";
RL Genetics 157:777-784(2001).
DR EMBL; AF278741; AAK13316.1; -.
FT NON_TER 1 1
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2924 MW; 4D23CB57E8C2A4B CRC64;

Query Match 2.2%; Score 45.5; DB 6; Length 25;
Best Local Similarity 47.8%; Pred. No. 2.9e+03;
Matches 11; Conservative 4; Mismatches 5; Indels 3; Gaps 1;

QY 14 LIGEL---PRLLLVLLCLPAVW 33
Db 3 LMGEVPSKPNLLFLMLPLNLW 25

RESULT 3
Q9R1C1 ID Q9R1C1 PRELIMINARY; PRT; 22 AA.
AC Q9R1C1;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Decay accelerating factor (Fragment).
GN DAF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c;
RX MEDLINE=99348049; PubMed=10417349;
RA Harris C.L., Rushmere N.K., Morgan B.P.;
RT "Molecular and functional analysis of mouse decay accelerating
RT factor.";
RL Biochem. J. 341:821-829(1999).
DR EMBL; AF143541; AAD51449.1; -.
FT NON_TER 1 1
FT NON_TER 22 22
SQ SEQUENCE 22 AA; 2371 MW; 3DAD8BF3A02D33DB CRC64;

Query Match 2.2%; Score 44.5; DB 11; Length 22;
Best Local Similarity 54.5%; Pred. No. 3e+03;
Matches 12; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 361 GHTC-ETLGLGLTGLTGMGLT 381
Db 1 GHTCLITLTVLHMLSLIGLYT 22

RESULT 4
Q71992 ID Q71992 PRELIMINARY; PRT; 29 AA.

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AC Q71992;
DT 01-AUG-1998 (T-EMBLrel. 07, Created)
DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Reverse transcriptase (Fragment).
OS Human endogenous retrovirus.
OC Viruses; Retroviral viruses; Retroviridae.
OX NCBI_TaxID=11827;
RN [1]
RP SEQUENCE FROM N.A.
RX Rose T., Schultz E.R., Henikoff J.G., Pietrokovski S., McCallum C.M.,
RA Henikoff S.;
RT "Consensus-degenerate hybrid oligonucleotide primers for amplification
RT of distantly-related sequences.";
RL Nucleic Acids Res. 0:0-0(1998).
DR EMBL; AF050505; AAC05560.1; -.
FT NON_TER 1 1
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3303 MW; CD65212FB4DB04AB CRC64;

Query Match 2.1%; Score 43; DB 15; Length 29;
Best Local Similarity 40.9%; Pred. No. 5.8e+03;
Matches 9; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

QY 109 LKQPYITONYFPVGTVEYECR 130
Db 1 LNSPTICQTY--VGQAIEFTCK 20

RESULT 5
Q96T45 ID Q96T45 PRELIMINARY; PRT; 20 AA.
AC Q96T45;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE MER receptor tyrosine kinase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20517330; PubMed=11062461;
RA Gal A., Li Y., Thompson D.A., Weir J., Orth U., Jacobson S.G.,
RA Apfelstedt-Sylla E., Vollrath D.;
RT "Mutations in MERTK, the human orthologue of the RCS rat retinal
RT dystrophy gene, cause retinitis pigmentosa.";
RL Nat. Genet. 26:270-271(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX Gal A., Li Y., Thompson D.A., Weir J., Orth U., Jacobson S.G.,
RA Apfelstedt-Sylla E., Vollrath D.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF366903; AAK54121.1; -.
KW Kinase; Receptor.
FT NON_TER 20 20
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2232 MW; A853BEF7EECE2910 CRC64;

Query Match 2.0%; Score 40.5; DB 4; Length 20;
Best Local Similarity 44.0%; Pred. No. 6e+03;
Matches 11; Conservative 2; Mismatches 3; Indels 9; Gaps 1;

QY 9 PAALPLLGELPRLLLVLLCLPAVW 33
Db 3 PAPLP-----LULGLFLPALW 18

RESULT 6
Q9JMC5 ID Q9JMC5 PRELIMINARY; PRT; 26 AA.
AC Q9JMC5;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)

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RN	[1]
RP	SEQUENCE.
RX	MEDLINE=92068458; PubMed=1367687;
RL	Uscategui E., Johansson G., Ek B., Pettersson G.;
RR	J. Biotechnol. 21:143-159(1991).
DR	InterPro; IPR000254; CBD_fungal.
PF	Pfam; PF00734; CBM_1; 1.
SQ	SEQUENCE 20 AA; 1939 MW; 3607F893BD532367 CRC64;
Query Match 1.9%; Score 40; DB 3; Length 20;	
Best Local Similarity 85.7%; Pred. No. 6.6e+03;	
Matches 6; Conservative 0; Mismatches 1; Indels 0;	
Qy	31 AVWGDCG 37
Dd	
	2 AVWGCG 8
RESULT 9	
O57555	PRELIMINARY; PRT; 27 AA.
ID	O57555;
AC	01-JUN-1998 (TrEMBLrel. 06, Created)
DT	01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DD	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	Hombobox protein LpHox9C (Fragment).
OS	Lampetra planeri (Brook lamprey).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OX	Petromyzontiformes; Petromyzontidae; Lampetra.
NCBI_TaxID=7750;	
[1]	
RP	SEQUENCE FROM N.A.
RX	MEDLINE=98358009; PubMed=9694633;
RL	Sharma A.C., Holland P.W.;
RR	"Estimation of Hox gene cluster number in lampreys.";
RD	Int. J. Dev. Biol. 42:617-620(1998).
DR	ENBL; AF044811; AAC03015.1; -.
FT	NON_TER 1
FT	NON_TER 27
SQ	SEQUENCE 27 AA; 2869 MW; 9F2AE2989CA319E1 CRC64;
Query Match 1.9%; Score 40; DB 13; Length 27;	
Best Local Similarity 72.7%; Pred. No. 9.7e+03;	
Matches 8; Conservative 1; Mismatches 2; Indels 0;	
Qy	42 VVNAQPALEGR 52
Dd	
	5 VPDAGPALRGR 15
RESULT 10	
O57554	PRELIMINARY; PRT; 27 AA.
ID	O57554;
AC	01-JUN-1998 (TrEMBLrel. 06, Created)
DT	01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DD	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	Hombobox protein LpHox9B (Fragment).
OS	Lampetra planeri (Brook lamprey).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OX	Petromyzontiformes; Petromyzontidae; Lampetra.
NCBI_TaxID=7750;	
[1]	
RP	SEQUENCE FROM N.A.
RX	MEDLINE=98358009; PubMed=9694633;
RL	Sharma A.C., Holland P.W.;
RR	"Estimation of Hox gene cluster number in lampreys.";
RD	Int. J. Dev. Biol. 42:617-620(1998).
DR	ENBL; AF044810; AAC03014.1; -.
FT	NON_TER 1
FT	NON_TER 27
SQ	SEQUENCE 27 AA; 2896 MW; 7517E29A4CA319FB CRC64;

```
Query Match      1.9%; Score 40; DB 13; Length 27;
Best Local Similarity 72.1%; Pred. NO. 9.7e+03;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 42 VPAQPALEGR 52
DB 5 VPDAGPALGR 15

RESULT 11
Q9JK06 PRELIMINARY; PRT; 30 AA.
AC Q9JK06
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (Fragment).
GN FBP2 OR FBPASE 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=20237676; PubMed=10773464;
RA Tillmann H., Stein S., Liehr T., Eschrich K.;
RT "Structure and chromosomal localization of the human and mouse muscle
fructose-1,6-bisphosphatase genes.";
RL Gene 247:241-253(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Stein S.;
RT "Mouse liver fructose-1,6-bisphosphatase: Gene structure,
transcriptional start point, chromosomal localization, cDNA cloning,
RT characterization of the recombinant protein, and analysis of tissue-
specific expression.";
RL Arch. Biochem. Biophys. 0:0-0(0).
DR EMBL; AJ243023; CAB90670.1; -.
DR HSSP; P00637; 1BK4.
DR MGD; MGI:95491; Fbp2.
DR InterPro; IPR000146; In_FB_phptase.
DR Pfam; PF00316; FBPhase; 1.
DR ProDom; PD001491; In_FB_phptase; 1.
KW Hydrolase.
FT NON_TER 1 1
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3014 MW; 55146C35C817E0C1 CRC64;

Query Match      1.9%; Score 40; DB 11; Length 30;
Best Local Similarity 42.1%; Pred. NO. 1.1e+04;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 193 GYKFGSTSSFCUIGSSV 211
DB 5 GYALGSAITVALSTGGV 23

RESULT 12
Q8N066 PRELIMINARY; PRT; 26 AA.
AC Q8N066
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE BAEBL (Fragment).
GN BAEBL.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
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RX MEDLINE=21996440; PubMed=12000842;
RA Blair P.L., Witney A., Haynes J.D., Moch J.K., Carucci D.J.,
RA Adams J.H.;
RT "Transcripts of developmentally regulated Plasmodium falciparum genes
RT quantified by real-time RT-PCR.";
RL Nucleic Acids Res. 30:2224-2231(2002).
DR EMBL; AF461093; AAM33517.1; -.
FT NON_TER 1 1
FT NON_TER 26 26
SQ SEQUENCE 26 AA; 3020 MW; D8C1933CAEE37D17 CRC64;

Query Match      1.9%; Score 39.5; DB 5; Length 26;
Best Local Similarity 29.6%; Pred. NO. 1e+04;
Matches 8; Conservative 5; Mismatches 9; Indels 5; Gaps 1;

QY 253 CNKGFTMIGEHSIYCTVNNDEGEWSGP 279
DB 4 CNNEYSM-----EYCTYSDESNSSPGP 25

RESULT 13
Q9BGJ0 PRELIMINARY; PRT; 25 AA.
AC Q9BGJ0
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ATP synthase beta subunit (Fragment).
OS Eulemur macaco macaco (Black lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Eulemur.
OX NCBI_TaxID=30603;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21100352; PubMed=11156996;
RA Schmitz J., Ohme M., Zischler H.;
RT "SINE Insertions in Cladistic Analyses and the Phylogenetic
RT Affiliations of tarsius bancanus to Other Primates.";
RL Genetics 157:777-784(2001).
DR EMBL; AF278740; AAK13315.1; -.
FT NON_TER 1 1
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 3023 MW; 4DE23CB5658D9A4B CRC64;

Query Match      1.9%; Score 39; DB 6; Length 25;
Best Local Similarity 53.3%; Pred. NO. 1.1e+04;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 19 PRELLLVLLCLPAVW 33
DB 11 PNNLLFLRLPLNW 25

RESULT 14
Q9IJ66 PRELIMINARY; PRT; 27 AA.
AC Q9IJ66
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Envelope protein (genome polypeptide) (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Alberto S.-F.;
RT "Influence of the dynamics of Hepatitis C virus quasispecies in the
RT histological outcome of liver transplantation.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF221229; AAF77791.1; -.
DR InterPro; IPR002531; HCV_NSI.
```

DR Pfam; PF01560; HCV_NSI; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 27 27
SQ SEQUENCE 27 AA; 2776 MW; CA21BB0A7FB6C40B CRC64;

Query Match 1.9%; Score 39; DB 12; Length 27;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 10; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

OY 352 TSGTTRLLSGHTCFILTLGLL 371
Db 4 TGGTV----GHNTFRLTSL 19

RESULT 15

O9XS67 PRELIMINARY; PRT; 28 AA.
AC O9XS67;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Very low density lipoprotein receptor (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99018030; PubMed=9799803;
RA Magrane J., Reina M., Pagan R., Luna A., Casaroli-Marano R.P.,
RA Angelin B., Gafvels M., Vilaro S.;
RT "Bovine aortic endothelial cells express a variant of the very low
RT density lipoprotein receptor that lacks the O-linked sugar domain."
RL J. Lipid Res. 39:2172-2181(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99283875; PubMed=10356983;
RA Magrane J., Casaroli-Marano R.P., Reina M., Gafvels M., Vilaro S.;
RT "The role of O-linked sugars in determining the very low density
RT lipoprotein receptor stability or release from the cell."
RL FEBS Lett. 451:56-62(1999).
DR EMBL; AF034420; AAD31591.1; --
KW Lipoprotein; Receptor.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 2855 MW; A407207D44718A54 CRC64;

Query Match 1.9%; Score 39; DB 6; Length 28;
Best Local Similarity 47.4%; Pred. No. 1.3e+04;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 295 TVQKPTTVNVPTTEVSPTS 313
Db 4 TVVNETKDTNTAEISPTS 22

Search completed: November 18, 2003, 07:49:22
Job time : 58 secs

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